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SIGNAL TRANSDUCING SYNAPTIC MOLECULES AND USES THEREOF

BACKGROUND OF THE INVENTION

CROSS-REFERENCE TO RELATED APPLICATIONS

The present application is a continuation of pending U.S. provisional application serial number 60/082,690 filed on April 22, 1998, and pending U.S. provisional application serial number 60/082,717 filed on April 23, 1998, the disclosures of both provisional applications fully incorporated herein by reference.

1. Field of the Invention

The present invention relates to signal transducing synaptic molecules and particularly to mammalian SYNGAP (Synaptic GTPase Activating Protein), including recombinant SYNGAPs and fragments and derivatives thereof. In one aspect, the invention provides molecules for detecting and analyzing SYNGAPs *in vitro* and *in vivo*. In another aspect, the invention provides assays for detecting compounds that modulate SYNGAP or SYNGAP-related activities. The invention has a variety of applications including use in screens to detect pharmacological agents useful in the diagnosis or treatment of disorders associated with SYNGAP.

2. Background

Neurons communicate by a variety of means including synaptic transmission. One form of synaptic transmission involves chemical signaling; a process generally involving neurotransmitter release from one neuron and modulation of a post-synaptic receptor in another neuron. The release and modulation is usually manifested by propagation of a chemical or electrical impulse. See Edelman, G.M. et al. (eds.) (1987) in *Synaptic Function,* New York: Wiley; and Goodman and Gilman (1996) in *The Pharmacological Basis of Therapeutics,* 9th ed. J.G. Hardman, et al. (eds) Pergamon Press, NY.

In many instances, chemical signaling requires specialized neuronal structures called chemical synapses. Analysis of chemical synapses has attracted substantial interest. For example, chemical synapses have been reported to be involved in many, if not all, nervous system functions including neuronal plasticity. In particular, neuronal plasticity is believed to impact critical functions such as cognition, e.g., memory and learning, as well as certain neurodegenerative disorders. See e.g., Kandel, E.R. et al; (1991) in *Principles of Neuroscience*, Appleton & Lange, Norwalk, CT and references cited therein.

A variety of approaches have been used in attempts to understand chemical synapses. For example, certain molecular and biochemical approaches have suggested that chemical synapses are structured and include molecules such as receptors, cytoskeletal proteins, and signal transduction molecules. See e.g., Ehlers, M.D., et al. (1996) *Curr. Opin. Cell Biol.* 8: 484; Sheng, M. (1996) *Neuron* 17:575; and Huganir, R.L. and Greengard, M. (1990) *Neuron* 5: 555.

More particularly, it has been reported that appropriate chemical synapse structure requires presence of a protein termed PSD-95/SAP90. The PSD-95/SAP90 protein is representative of a family of molecules including SAP120. Specific members of the PSD-95/SAP90 family are localized at or near chemical synapses. See e.g., Ehlers, M.D., et al. *supra*; Sheng, M *supra;* Lau, L. F., et al. (1996) *J. Biol. Chem.* 271:21622; Muller, B.M., et al. (1996) *Neuron* 17:255; and references cited therein.

There has much effort towards understanding PSD-95/SAP90 and related proteins. For example, it has been reported that most members of the protein family exhibit the same or a closely related structure, i.e., three tandem PDZ (PSD-95, DLG, ZO-1) domains, a SH3 (src homology 3) domain, and an inactive yeast guanylate kinase domain (GK). See e.g., Kim, E., et al. (1995) *Nature* 378:85; Kornau, H. C., et al. (1995) *Science* 269:1737.

There has been recognition that PDZ domains exist in proteins associated with cell membranes. For example, it has been reported that the PDZ domains of PSD-95 bind to specific subunits of the (N-methyl-D-aspartate) NMDA receptor. It has also been reported that the last three amino acids of the NMDA receptor subunits define a consensus sequence (T/SXV; X is any amino acid). The subunit sequence has been reported to facilitate the binding. See e.g., Kennedy, M. B. (1995) *Trends Biochem. Sci.* 20; Gomperts, S. N. (1996) *Cell* 84:659; Sheng, M. *supra*.

There has also been recognition that chemical synapses can employ signal transduction to modulate pre- and post-synaptic activity. For example, certain members of the PSD-95/SAP90 protein family are believed to be associated with signal transduction. More particularly, the PSD-95 protein has been proposed to interact with certain signal transduction kinases. That interaction has been proposed to be important to synaptic function. See Gomperts, *supra*; Saras, J., and Heldin, C. H. (1996) *Trends Biochem. Sci.* 21:455; Huganir, R.L. and Greengard, M. *supra*.

There has also been recognition that the PSD-95/SAP90 protein may be capable of serving as an adaptor molecule. More specifically, there have been reports that the PSD-95/SAP90 protein may be able to relate synaptic activity and signal transduction in some instances. That property is believed to important to appropriate synapse function. See e.g., Brenman, J.E. et al. (1996) *Cell* 84: 757; and Saras, J. and Heldin, Carl-Henrik (1996), *supra*.

A variety of signal transduction molecules are known including specified kinases and proto-oncogenes. For example, the proto-oncogene Ras is recognized as a G-protein that is apparently involved in signal transduction pathways affecting, e.g., cell growth, cell differentiation, neuronal plasticity and cell survival. In particular, Ras appears to have a substantial role in kinase activation. In addition, biological activity manifested by a variety of neurotrophic factors (i.e. neurotrophins) may be derived through Ras-

associated signaling pathways. See e.g., Bokoch, G. M., and Der, C. J. (1993) *FASEB. J.* 7:750; Marshall, C. J. (1996) *Cell Biol.* 8:197; Finkbeiner, S. and Greenberg, M.E. (1996) *Neuron* 16:233; Kang, H., and Schuman, E. M. (1996) *Science* 273:1402.

Certain neuronal functions have been proposed to be affected by Ras-mediated signal transduction. See e.g., Seger, R., and Krebs, E. G. (1995) *FASEB J.* 9:726; and Finkbeiner and Greenberg, *supra*.

Additional signal transduction pathways are known. For example, the inositol triphosphate signaling pathway has been reported to couple modulation of certain receptors to a variety of functions, many of which relate to calcium. See e.g., Berridge, M.J. (1988) *Pro. R. Soc. Lond. (Biol.)* 234: 359.

It would be desirable to identify molecules that impact chemical synapse function and particularly interact with the PSD-95/SAP90 protein. It would be further desirable to identify molecules that can bind the PSD-95/SAP90 protein and affect signal transduction. It would also be desirable to have effective assays for identifying compounds and especially pharmaceutical agents with capacity to modulate the function of these molecules.

SUMMARY OF THE INVENTION

The present invention features molecules that relate to SYNGAP (Synaptic GTPase Activating Protein); an excitatory synapse protein that has been found to bind synaptic proteins and modulate signal transduction. In one aspect, the invention provides isolated polynucleotides that encode SYNGAP or fragments or derivatives thereof. Further provided are SYNGAP or SYNGAP-related polypeptide encoded by the polynucleotides. In another aspect, the invention provides immunological molecules that are capable of binding the polypeptides. Additionally provided are methods for using the molecules of this invention, e.g., to treat or prevent at least one disorder mediated by

SYNGAP. The invention also provides screening assays for detecting compounds useful in the diagnosis or treatment of disorders impacted by SYNGAP.

We have discovered mammalian SYNGAP: a novel protein that binds synaptic proteins important for chemical synapse function. Additionally, we have found that SYNGAP is capable of modulating certain signal transduction molecules and particularly the Ras proto-oncogene (Ras). We have particularly found that SYNGAP is positioned to relate synaptic activity and signal transduction, thereby indicating a significant role in many aspects of nervous system function.

As will be discussed below, SYNGAP is represented by a family of alternatively spliced variants including SYNGAP-a, SYNGAP-b, and SYNGAP-c.

The present invention provides a number of significant uses and advantages. For example, the invention relates, for the first time, recognized synaptic proteins such as PSD95/SAP90 and SAP120 to signal transduction. More particularly, the invention provides SYNGAP and SYNGAP-related molecules that are believed to serve as adaptors between key synaptic proteins and specific transduction pathways. Accordingly, the present invention is expected to facilitate attempts to more fully understand relations between synapses and signal transduction, particularly relationships between synaptic function and signaling molecules such as Ras, inositol triphosphate and certain other transduction molecules.

The present invention has a wide spectrum of important applications. For example, specific molecules of this invention can be used as a diagnostic tool to detect excitatory synapses, i.e., those that include mammalian SYNGAP. Illustrative of such excitatory synapses are those impacting neuronal plasticity, particularly habituation, sensitization, learning and memory; as well as certain neurological disorders. In addition, the invention can be employed in the diagnosis, treatment or prophylaxis of certain neurological disorders impacted by SYNGAP. As will be discussed in more detail below,

exemplary neurological conditions include those specifically affecting awareness and cognition as well as neuronal growth and survival.

Further, the present invention provides a variety of highly useful molecular markers including polynucleotides, polypeptides, and immune system molecules that can be used in many commercial, medical, home or research settings. For example, certain molecules of this invention can be used in screening assays to detect compounds and particularly pharmaceutical agents useful in the diagnosis or treatment of neurological disorders impacted by SYNGAP. Of particular interest are recognized manipulations that can be employed for the identification of small molecules, e.g., synthetic peptides, peptide mimetics, drugs, etc., that can modulate interaction between SYNGAP and the synaptic proteins to which it associates; interaction between SYNGAP and signal transduction molecules or both. Related techniques can be used to screen for small molecules that potentially block or enhance one or all of these interactions. In particular, *in vitro* screens are provided that can detect SYNGAP antagonists or agonists.

Additional uses include use of SYNGAP polynucleotides to detect SYNGAP expression in desired cells or groups of cells such as tissue or an organ by conventional *in situ* hybridization methods.

Particularly useful are SYNGAP-binding immune system molecules of this invention such as the antibodies and antigen-binding antibody fragments provided below. For example, the antibodies (monoclonal and polyclonal) can be used alone or in combination with other agents to facilitate identification of excitatory chemical synapses that include SYNGAP. In some instances, it may be desirable to include the antibodies wholly or as part of a therapeutic strategy to monitor or in some cases modulate the excitatory chemical synapses. Preferred molecules of the invention are flexible and can be modified, if desired, to deliver a desired molecule such as a drug, toxin, enzyme or radionuclide optionally through a linker sequence such as a peptide linker sequence. As

an illustration, a SYNGAP binding antibody of this invention can be detectably-labeled to identify excitatory chemical synapses *in vitro* or *in vivo*.

The SYNGAP and SYNGAP-related molecules of this invention have additional uses and advantages *in vitro* and *in vivo*. For example, the molecules can be employed in functional, cellular and molecular assays (e.g., screens) and in structural analysis, including X-ray crystallography, nuclear magnetic resonance imaging (NMRI), computational techniques. Of particular interest are those techniques involving computer-assisted simulation of synapses (i.e. formulation of virtual synapses). Also included are useful techniques for using the SYNGAP and SYNGAP-related molecules as markers that can provide diagnostic imaging of excitatory chemical synapses *in vivo*. By way of illustration, certain molecules of this invention can be employed to visualize specific neurons and particularly chemical synapses including SYNGAP in the brain of a living patient. In this embodiment, the desired molecule will usually be detectably-labeled with a suitable tag such as a radionuclide or other suitable imaging component known in the field.

Specific SYNGAP and SYNGAP-related molecules of this invention can be provided in a kit form or other convenient form to facilitate manufacture, packaging, dissemination, storage, and/or use of the present invention.

Accordingly, in one aspect, the invention provides isolated polynucleotides (RNA, mRNA, cDNA, genomic DNA, or chimeras thereof) that encode SYNGAP or a fragment or derivative of SYNGAP. Illustrative of such polynucleotides include those encoding a mammalian SYNGAP, e.g., a primate and particularly a rat or a human SYNGAP. In one embodiment, the polynucleotide encodes a mammalian SYNGAP having a molecular weight of between about 100 to about 150 kDa or greater. In another embodiment, the polynucleotide has at least about 70 percent sequence identity to any of the nucleotide sequences shown in SEQ ID NOS. ~~1-2, 4-5, or 7-8~~ 1, 3, or 5. Such sequence similarity (i.e. about 70%) or greater similarity will sometimes be referred to herein as

"substantial homology" or like term. Specifically preferred polynucleotides of the invention encode the rat SYNGAP shown in any of the SEQ ID Nos. ~~3, 6, or 9~~ 2, 4, or 6.

In another aspect, the present invention provides an isolated polynucleotide that is capable of hybridizing to the nucleotide sequence shown n SEQ ID Nos. 1-2, 4-5, or 7-8 under moderate stringency hybridization conditions. In a preferred embodiment, the polynucleotide will also hybridize to those specific sequences shown in SEQ ID NOS. 1-2, 4-5, or 7-8 under high stringency conditions. The terms "moderate" and "high" hybridization stringency have readily understandable meaning to those of skill in this field. Exemplary stringency conditions are disclosed in the discussion and examples which follow. In one embodiment, the polynucleotide capable of hybridizing to the SEQ ID NO: 1 or ~~SEQ ID NO: 2~~ under high stringency conditions is between from about 12 to about 50 nucleotides in length. Illustrative of such polynucleotides are oligonucleotide primers made by conventional synthetic methods. In another embodiment, the polynucleotide is between about 100 to about 3500 nucleotides in length or greater. Illustrative of such polynucleotides are restriction enzyme fragments or chemically synthesized fragments complementary to the sequences shown in SEQ ID Nos. ~~1-2, 4-5, or 7-8~~ 1, 3, or 5.

In another embodiment of the invention, the polynucleotide capable of hybridizing to the nucleotide sequence shown in SEQ ID Nos. ~~1-2, 4-5, or 7-8~~ 1, 3, or 5 under high stringency conditions has a length of between about 100 up to about 4000 nucleotides or greater. In a preferred embodiment, the polynucleotide is a cDNA encoding an amino acid sequence capable of modulating the proto-oncogene Ras as determined, e.g., by a standard Ras GTPase activity assay. In a specific embodiment, the amino acid sequence encoded by the polynucleotide is capable inhibiting the Ras protein by at least about 10% up to about 100% in the standard Ras GTPase assay. Additionally preferred are polynucleotides that encode polypeptides capable of modulating Ras-mediated signaling transduction pathways and optionally signal transduction molecules "downstream" of Ras (directly or indirectly). Examples of such downstream molecules include recognized

signaling and effector molecules. Illustrative methods for identifying such polynucleotides and amino acid sequences are described below.

One or a combination of standard approaches can be used to monitor Ras GTPase activity in cells or cell lysates. Preferably, the cell or cell lysate will include a naturally-occurring or recombinant Ras protein. Preferred assays for measuring and quantitating the Ras GTPase activity are discussed below.

Additionally preferred polynucleotides of this invention encode a mammalian SYNGAP or fragment or derivative thereof that is capable of significantly reducing inositol triphosphate signaling as determined, e.g., by modulation of phospholipase C activity in a standard phospholipase C enzyme assay. Preferably, the polynucleotide is a cDNA that is capable of increasing or decreasing the enzyme activity by at least about 10% or more up to about 100% relative to a suitable control assay. Specific phospholipase C assays are described below.

Additionally preferred polynucleotides of this invention encode a mammalian SYNGAP or a SYNGAP-related amino acid sequence that is capable of binding at least from about 1, 2 or 3 up to about 10 PDZ domains as determined by a standard PDZ domain binding assay. As noted above, the PDZ domain has been reported to be present in a variety of membrane proteins, e.g., the PSD95/SAP90 and SAP120 proteins, and is believed to significantly impact chemical synapses.

By the term "SYNGAP-related" nucleotide or amino acid sequence or similar term is meant a fragment or derivative of SYNGAP sequence (polynucleotide or polypeptide as described below.

A variety of methods are known in this field for detecting and quantifying, if desired, PDZ binding. In general, the methods are capable of detecting formation of a binding complex and can be optimized to provide qualitative or quantitative

characterization of those binding complexes. Illustrative methods for detecting the PDZ binding are more fully disclosed in the discussion and examples that follow.

Additionally preferred polynucleotides are those molecules that encode an amino acid sequence that includes at least a Ras GTPase Activating Protein (GAP) domain up to about 2 to about 3 GAP domains, and a C-terminal sequence that includes at least the following general amino acid sequence: (T or S), X V; wherein X is an amino acid, preferably one of the 20 natural amino acids.

Further preferred are those polynucleotides that encode an amino acid sequence that includes at least one pleckstrin homology (PH) up to about 3 PH domains and at least one C2 domain up to about 3 C2 domains.

Particularly preferred polynucleotides of this invention encode an amino acid sequence that includes in an N- to C-terminal orientation: at least one PH homology, preferably one PH homology; at least one C2 domain, preferably one C2 domain; at least one GAP domain, preferably one GAP domain; and the C-terminal sequence having the sequence (T or S), X V described above. Additionally preferred is a polynucleotide encoding an amino acid sequence that includes in an N- to C-terminal direction at least about the following amino acids of SEQ ID NO. 6: 4 to 72, 87 to 190, 266 to 502 and 1132 to 1135.

Specifically preferred are those polynucleotides that encode a rat SYNGAP as represented by any one of SEQ ID NOS. 2 4 or 6 ~~3, 6 or 8~~ including fragments or derivatives thereof.

One or a combination of different strategies can be used to analyze the SYNGAP or SYNGAP-related molecules disclosed herein, e.g., to detect homologous molecules or to identify protein domains (e.g., GAP, PH, and C2). Specifically included are

biochemical, immunological and biosensor-type assays as well as certain well-known computer-assisted manipulations.

Additionally provided by the present invention are fragments or derivatives of the polynucleotides encoding mammalian SYNGAP or SYNGAP-related molecules, as well as recombinant vectors including the polynucleotides or the fragments or derivatives thereof. It is generally preferred that the recombinant vector be capable of propagating the isolated polynucleotide in a suitable prokaryotic or eukaryotic host cell. Additionally preferred recombinant vectors are capable of expressing that isolated polynucleotide as RNA and preferably mRNA, in a suitable cell expression system. The recombinant vector can include nearly any number of useful elements, however in most cases the vector will include control elements operably linked to the inserted nucleic acid (e.g., promoter, leader, and/or enhancer elements) which control elements can be selected to optimize replication and/or transcription of the vector in the cells.

As noted, polynucleotides of the invention generally encode mammalian SYNGAP or a fragment or derivative thereof. In one embodiment, the polynucleotides are substantially homologous to the SYNGAP sequence shown in SEQ ID NO: ~~3, 6 or 9~~ 2, 4 or 6. In a specific embodiment, the isolated polynucleotides include or consists of cDNA and have a length of between about 50 to about 100 nucleotides up to about 4000 nucleotides or more, as determined by standard nucleic acid sizing methods. In another embodiment, the isolated nucleic acid includes or consists of RNA and particularly mRNA that is also substantially homologous to the specific rat SYNGAP sequence and which can have substantially the same length as the cDNA.

Also provided are host cells that include a polynucleotide as disclosed herein including those that express SYNGAP, a SYNGAP-related molecule or a fragment or derivative thereof under suitable cell culture conditions. Preferably, the host cells are capable of expressing the desired amino acid sequence in the host cell, cell medium, or both.

The invention also includes methods for isolating a polynucleotide encoding a mammalian SYNGAP or SYNGAP-related molecule such as the rat SYNGAP sequence specifically described below. In general, the methods include introducing the polynucleotide into host cells, typically as a recombinant vector including the polynucleotide, culturing the host cells under conditions suitable for propagating the polynucleotide and purifying the polynucleotide from the host cells to obtain larger portion of the isolated polynucleotide therefrom. Host cells useful for propagating the polynucleotides and/or polypeptides of this invention can be eukaryotic, prokaryotic, more particularly, fungal, yeast, animal or insect as desired. Host cells amenable for large scale production of mammalian SYNGAP are especially useful for commercial and industrial applications. Alternatively PCR amplification or related amplification methods can be used to isolate the polynucleotide.

Further provided are cultured host cells which have been transformed, transfected or infected either transiently or stably by at least one recombinant vector of the invention which vector includes an isolated polynucleotide that encodes a mammalian SYNGAP or a fragment or derivative thereof (DNA or RNA).

Recombinant vectors of the invention can be introduced into suitable cells or groups of such cells including tissue or organs if desired either *in vitro* or *in vivo*. Preferably, the cells are capable of expressing the recombinant vector at detectable levels. Host cells comprising the vectors can be cultured in medium capable of supporting propagation and/or expression of the vectors in the cells. The cells can be eukaryotic cells, preferably mammalian cells such as neurons and neuron-associated cells (e.g., glia) which cells are capable of expressing desired sequences in the recombinant vector. The cells can be primary cells or the cells can be immortalized. In some instances it will be desirable to introduce the vector into a suitable prokaryotic host e.g., bacteria, insect, yeast or fungal cells to propagate the vector.

The present invention also provides useful oligonucleotide primers, typically single-stranded primers, which oligonucleotide primers are complementary to a polynucleotide encoding a mammalian SYNGAP. For example, in one embodiment, the oligonucleotide primers are complementary to the rat SYNGAP sequence shown in any one of SEQ ID Nos. ~~1-2, 4-5, or 7-8~~ 1, 3 or 5. The oligonucleotide primers have a variety of useful applications, e.g., to detect or amplify a mammalian SYNGAP of interest. Exemplary oligonucleotide primers will generally have length of between about 12 to about 70 nucleotides although somewhat larger or smaller primers are useful for some applications.

Additional polynucleotides of the present invention have important uses. For example, as discussed, the invention provides for recombinant vectors that include an isolated polynucleotide relating to SYNGAP. Specific recombinant vectors can be used to produce significant amounts of nucleic acid sequence that can be sense or anti-sense, single-stranded or double-stranded as needed. Generally, RNA transcribed from DNA is referred to as the "sense" RNA strand and oppositely oriented RNA is termed antisense RNA. Antisense polynucleotides, then, refer to sequences of DNA or RNA which can bind in a Watson-Crick fashion to a sequence on a target mRNA. See generally Bentley, D. L. and Groudine, M. (1986) *Nature* 321:702; and Kimelman, D. *Gene regulation: Biology of Antisense RNA and DNA*, R. P. Erickson, J. G. Izant, eds. (Raven Press, New York).

Mammalian SYNGAP RNA and particulary a SYNGAP mRNA existing in a biological sample such as in an excitatory chemical synapse (*in vivo* or *in vitro*) will sometimes be referred to herein as a "target" to denote potential for specific binding between a polynucleotide of interest, e.g., a suitable anti-sense RNA, and the SYNGAP mRNA in the sample.

In one preferred embodiment, the recombinant vectors include DNA sequences that encode an anti-sense RNA which RNA is substantially homologous to mammalian

SYNGAP polynucleotides of this invention e.g., a rat SYNGAP. It is preferred that the recombinant vectors include cDNA sequences. In this instance it will be understood that the anti-sense RNA will usually include a uracil (U) in place of thymidine (T) where the cDNA sequence has a thymidine. In a preferred embodiment, the anti-sense RNA has a length of at least about 20 to about 50 nucleotides, at least about 100 to about 250 nucleotides, at least about 300 to about 700 nucleotides, at least about 1000 to about 2000 nucleotides and up to about 2500 to about 4000 nucleotides as determined by standard polynucleotide sizing methods. In most cases, the length of the anti-sense RNA will be guided by intended use including the length of the target and the level of anti-sense suppression desired.

The antisense RNA encoded by specific recombinant vectors of this invention is usually designed to undergo complementary base pairing (hybridization) with the target, rendering the target essentially unavailable for translation in most cases. In some instances, the antisense RNA will render the target susceptible to degradation, thereby substantially reducing the amount of the target in relevant cells or tissue. Accordingly, the recombinant vectors of the invention can be used to control the synthesis and/or expression of SYNGAP in desired neurons *in vitro* or *in vivo*.

Specific recombinant vectors of this invention that are capable of producing anti-sense RNA complementary to a mammalian SYNGAP mRNA (or more than one of such mRNA) can be used therapeutically to reduce levels of the target *in vivo* or *in vitro*. For example, in one embodiment, a desired recombinant vector is administered to a patient suffering from or suspected of suffering from a SYNGAP related disorder such as those specified herein. In this instance, the patient will benefit from substantially reduced or totally absent levels of the target. Preferred administration is sufficient to reduce levels of the target mRNA in the patient. Efficacy of the technique can be monitored and quantified if desired by a variety of techniques including Northern and Western blotting.

In another embodiment, the recombinant vector is formatted to produce anti-sense DNA of about the same size as the anti-sense RNA.

In addition, the polynucleotides of this invention and particularly the isolated nucleic acids and recombinant vectors described herein can be used as important controls for detecting and analyzing normal and aberrant mammalian SYNGAP expression *in vitro* and *in vivo*.

In another aspect, the present invention provides isolated mammalian SYNGAP preferably having an apparent molecular weight of between about 100 to about 150 kDa. The molecular weight of the SYNGAP can be determined by a variety of standard means including polyacrylamide gel electrophoresis. Preferred are polypeptide sequences having at least about 200 amino acids up to about 1000 amino acids or greater including about 1100 amino acids. Specifically provided is rat SYNGAP as shown at the amino acid sequence level in any one of SEQ ID NOS. ~~3, 6 or 9~~ 2, 4, or 6.

In another aspect, there is provided an isolated polypeptide having at least about 70 percent amino acid sequence homology to the sequence illustrated in SEQ ID NO: ~~3, 6~~ 2, 4, or ~~9~~ 6. Additionally provided are isolated fragments or derivatives of that polypeptide.

The invention also provides methods for producing a mammalian SYNGAP in which the method includes culturing the host cell in medium under conditions suitable for expression of the SYNGAP in the host cell or medium.

In another aspect, the present invention provides an antibody or antigen-binding fragment thereof capable of binding the amino acid sequence shown in SEQ ID NO. ~~9~~ 6. Preferably, the binding of the antibody or antigen-binding fragmeent is blocked by at least about 80%, 90% or more up to about 100% by contact with the amino acid sequence shown in SEQ ID NO:21 or a sequence substantially homologous thereto. The percent

blocking by the amino acid sequence can be determined by a variety of means including a conventional immunoprecipitation assay or a Western immunoblot.

In one preferred embodiment, the antibody is a capable of binding excitatory synapses as determined by microscopy. In this embodiment, the antibody can be a monoclonal or a polyclonal antibody or an antigen-binding fragment thereof. In most cases, the antibody or antigen-binding fragment will be detectably-labeled or will be capable of generating a detectable label as specified below to help visualize and optionally quantitate synaptic binding.

Additionally, the invention pertains to methods for making specific immune system molecules and particularly antibodies (polyclonal, monoclonal or chimeric molecules) which bind certain SYNGAP or a SYNGAP-related molecules described herein. The methods generally include using a substantially purified sample of a desired SYNGAP polypeptide, as immunogen. Exemplarly antibodies are monoclonal antibodies obtained by conventional hybridoma manipulations. The antibodies can also be generated from an immunogenic peptide that comprises one or more epitopes of the polypeptide. It will be useful in some settings to covalently attach a suitable cytotoxic, anti-metabolic, or detectable label to the antibody by methods well-known in the field to help detect and/or modulate desired synapses that include mammalian SYNGAP and particularly human or rat SYNGAP *in vitro* or *in vivo*.

It will be understood that an "immune system molecule" generally relates to antibodies and antigen-binding fragments of those antibodies that are derived from the immune system of a mammal such as a mouse, rat, rabbit, human, and the like.

The immune system molecules of this invention provide a number of uses and advantages. For example, the immune system molecules can be used to modulate mammalian SYNGAP expression *in vitro* or *in vivo*, e.g., by employing conventional microinjection techniques. In one approach, a suitable amount of a desired SYNGAP

antibody is suspended in a physiologically acceptable buffer and injected into a desired cell or group of cells including tissue or an organ, which amount is sufficient to reduce or eliminate SYNGAP expression as determined, e.g., by the biochemical and functional assays described herein. In some instances, such approaches will be well-suited to modulate SYNGAP function, e.g., to impact neuronal plasticity *in vitro* or *in vivo*.

In another aspect, the present invention provides a kit that typvically includes at least one container means comprising at least one of: 1) an antibody or antigen-binding fragment thereof capable of binding mammalian SYNGAP, 2) an isolated polynucleotide comprising sequence with at least about 70% sequence homology to any one of the sequences shown in SEQ ID NOs: 1~~, 2, 4, 5, or 7~~ 3, 8, 5; 3) a pair of oligonucleotide primers capable of hybridizing to any one of the sequencs shown in SEQ ID NOs: 1~~, 2, 4, 5, or 7~~ 3, 8, 5; ~~8,~~ preferably under high stringency conditions; and 4) a polypeptide with at least about 70% to about 100% sequence homology to the sequence shown in any one of the sequences shown in SEQ ID NOs: ~~3, 6~~ 3, 4, 6 or ~~9~~ or a fragment or a derivative thereof.

In one embodiment, the kit includes a system for: 1) treating or preventing a disorder in a mammal associated with the SYNGAP, 2) detecting excitatory synapses in a cell or group of cells *in vitro* or *in vivo* , or both.

Isolated polynucleotides and polypeptides of the invention can be obtained as a substantially pure preparation if desired. That is, the nucleic acids and polypeptides can be isolated in substantially pure form by standard methods and can be provided as sterile preparations if desired. Methods for providing substantially pure preparations of nucleic acids and polypeptides are discussed below.

In another aspect of the present invention, there is provided methods for modulating excitatory synapse function in a cell or group of cells *in vitro* or *in vivo*. In this embodiment, the method includes administering to the cells a modulation effective amount of at least one polynucleotide of this invention or fragment or derivative thereof.

By the term "modulation effective" is meant a change in exciting synapse function (e.g., amout of SYNGAP).

The present invention also includes methods for modulating excitatory synapse function in a cell or group of cells *in vitro* or *in vivo*. In this embodiment, the method includes administering to the cells a modulation effective amount of a mammalian SYNGAP of this inveniton, including a fragment or derivative thereof.

In embodiments of the methods for modulating excitatory synapse function, the modulation can include an increase in excitatory synapse number. Excitatory synapses can be visualized and quantified, if desired, by a variety of means including microscopy or centrifugation.

In another aspect, the present invention includes methods for treating a disorder associated with a mammalian SYNGAP including administering to a patient suffering from or susceptible to such disorder an effective amount of at least one isolated polynucleotide of this invention or fragment or derivative thereof.

Additionally provided are methods for treating a disorder associated with a mammalian SYNGAP comprising administering to a patient suffering from or susceptible to such disorder an effective amount of an isolated SYNGAP of this invention or fragment or derivative thereof.

In embodiments of the methods for treating SYNGAP-related disorders, the disorder can be a neurological disorder of the central (CNS) or peripheral (PNS) nervous system. In a specific embodiment, the CNS disorder is at least one of an affective disorder, a cognitive disorder, or a neurodegenerative disorder. For example, the affective disorder can be depression; the cognitive disorder can be at least one of memory loss, a learning disability, or schizophrenia; and the learning disability can be attention deficit disorder (ADD). In another specific embodiment, the degenerative disorder can be

at least one of Parkinson's disease (PD), Huntington's disease (HD), senile dementia, or Alzhemier's disease (AD). In a further specfiic embodiment, the PNS disorder is amyotrophic lateral sclerosis. In another specific embodiment, the neurological disorder is associated with at least one of trauma, an immune response or ischemia.

The methods for treating or preventing the SYNGAP-related disorders will also find applicability in the manipulation of habituation, sensitization, learning and memory in research settings.

As noted, the present invention provides a variety of screening assays for detecting compounds and especially pharmaceutical agents for use in the diagnosis or treatment of disorders impacted by mammalian SYNGAP.

In one embodiment, there is provided methods for identifying a compound useful in the diagnosis or treatment of a disorder relating to the SYNGAP. In a specific embodiment, the method includes at least one of the following steps:

a) culturing cells capable of forming synapses comprising SYNGAP under conditions conducive to forming or maintaining synapses,

b) contacting the cells with a candidate compound,

c) analyzing the cells for an increase or decrease in the number of synapses; and

d) detecting the increase or decrease as indicative of the compound useful in the diagnosis or treatment of the disorder relating to SYNGAP.

In another embodiment, the invention provides methods for detecting a compound capable of modulating a Ras-activated second messenger pathway. In this embodiment, the method includes at least one of the following steps:

a) providing a Ras response system comprising a recombinant mammalian GTPase Activating Protein at Synapses (SYNGAP),

b) contacting the Ras response system with a candidate compound,

c) analyzing the Ras response system for an increase or decrease in Ras activity; and

d) detecting the increase or decrease in the Ras activity as indicative of the compound capable of modulating the Ras-activated second messenger pathway.

In preferred embodiments, the Ras response system which includes at least one of Ras a nucleotide di- or tri-phosphate; adenylate cyclase; and an isolated polynucleotide encoding the SYNGAP or a fragment or a derivative thereof. The Ras response system can be provided by one or a combination different strategies including being provided in a host cell or a group of host cells (e.g., tissue or an organ), or a lysate of the cells, tissue or organ.

In another embodiment, the invention includes methods for detecting a compound capable of modulating a Ras-Raf (MAP kinase) cascade. The RAS-GTPase activating activity of SYNGAP can be measured using the MAP kinase as a reporter in a suitable primary or cultured cells. In this embodiment, the method includes at least one of the following steps:

a) transfecting a cells with a reporter gene construct capable of being modulated by Ras-Raf (MAP kinase),

b) transfecting the cells with a polynucleotide encoding any one of the SYNGAP sequences shown in SEQ ID Nos. ~~3, 6, or 9~~ 24 6,

c) contacting the cells with a candidate compound; and

d) detecting the reporter gene construct as being indicative of the compound capable of modulating the RasGTPase activity of SYNGAP.

It will be appreciated that in some embodiments of the method, the SYNGAP cDNA can be provided before, during or after transfection of the reporter gene construct.

In another embodiment, the invention includes methods for detecting a compound capable of modulating a phospholipid-activated second messenger pathway. In this embodiment, the method includes at least one of the following steps:

a) providing an inositol triphosphate response system comprising a recombinant SYNGAP,

b) contacting the inositol triphosphate response system with a candidate compound,

c) analyzing the inositol triphosphate response system for an increase or decrease in phospholipase activity; and

d) detecting the increase or decrease in the phospholipase activity as indicative of the compound capable of modulating the phospholipid-activated second messenger pathway. In preferred embodiments, the phospholipase is a phosphoinositide-specific enzyme such as phospholipase C.

In one embodiment of the method, the inositol triphosphate response system further includes at least one of phosphatidylinositol (PI) and an isolated polynucleotide encoding the SYNGAP or a fragment or a derivative thereof. In a specific embodiment, the inositol triphosphate response system includes at least one of diacylglycerol, protein kinase C, and inositol 1,4,5 triphosphate ($INSP_3$). In a related embodiment, the phospholipid-activated second messenger pathway is capable of at least one of calcium (Ca^{+2}) release or protein phosphorylation. The inositol triphosphate response system can be provided by one or a combination different strategies including being provided in a host cell or a group of host cells (e.g., tissue or an organ), or a lysate of the cells, tissue or organ.

In another embodiment of the method, at least the pleckstrin (PH) homology of SYNGAP is provided for use with the inositol triphosphate response system. In another embodiment of the method, at least the PH homology and the SYNGAP C2 domain is used with the inositol triphosphate response system.

Additionally provided by the present invention are methods for detecting a compound capable of modulating phospholipid-dependent calcium (Ca^{-2}) binding to at least the SYNGAP C2 domain. In this embodiment, the method includes at least one of the following steps:

a) mixing a phospholipid, calcium (Ca^{+2}) and at least the SYNGAP C2 domain, the mixing being under conditions conducive to forming a complex,

b) contacting the mixture with a candidate compound,

c) analyzing the mixture for formation of the complex; and

d) detecting the complex as indicative of the compound capable of modulating the phospholipid-dependent binding between the calcium (Ca^{+2}) and at least the C2 domain of SYNGAP.

In another embodiment of the method, at least the PH homology and the SYNGAP C2 domain is used with the inositol triphosphate response system.

In embodiments of the present invention in which use of rat SYNGAP is desired, it will be possible to use a polypeptide sequence that includes and preferably consists of the sequence represented by any one of SEQ ID Nos : 3, 4, 6 or 8. Also contemplated are embodiments of the present invention which include use of a fragment or a derivative of the rat SYNGAP sequence as show in SEQ ID NOs: 3, 4, 6 or 8.

The methods for detecting the compound capable of modulating the phospholipid-activated second messenger pathway are flexible and can be used if one or more components of the inositol triphosphate response system, e.g., PI, act "upstream" or "downstream" of SYNGAP.

In another embodiment of the present invention, there is provided methods for detecting a test amino acid sequence capable of binding a mammalian SYNGAP. In one embodiment, the method includes contacting the test amino acid sequence with the mammalian SYNGAP or a binding fragment or the derivative thereof under conditions

conducive to forming a complex; and detecting the complex as indicative of the test amino acid sequence capable of binding the SYNGAP. For example, in a specific embodiment, the mammalian SYNGAP can be the rat SYNGAP sequence shown in SEQ ID NO: 6 or a suitable fragment or derivative thereof. Detection of the binding can be acomplished by one or a combination of different strategies such as at least one of immunoprecipitation, affinity chromatography, or a suitable biosensor assay.

In another embodiment of the method for detecting a test amino acid sequence capable of binding a mammalian SYNGAP, the contacting step can be performed in cells and the detecting step can include monitoring expression of a detectable gene product expressed by the cells In a preferred embodiment, the steps are performed in yeast cells. Particulary preferred are those yeast cells (strains) that are suited for performing what is generally known in the field as a "two-hybrid" assay or a related term. In other embodiments, the detecting step of the methods can include screening a polypeptide expression library or a combinatorial peptide library, e.g., by a hybridization type assay using a suitable polynucleotide of this invention, for the test amino acid sequence.

In preferred instances, the methods for detecting the binding between the test amino acid sequence and the SYNGAP will typically register binding between at least one PDZ domain in the test amino acid sequence and a C-terminal sequence in the SYNGAP or fragment or derivative thereof. Preferably, the C-terminal sequence has the following general sequence: (T or S) XV; wherein X is an amino acid as defined below. The SYNGAP sequence used can be the rat SYNGAP sequence disclosed in SEQ ID NO: 2, 4 or 6 as well as suitable fragments or derivatives of that sequence.

Additionally provided are amino acid sequences detected by any of the methods for detecting the test amino acid sequence capable of binding a mammalian SYNGAP.

The present invention includes, in another aspect, methods for detecting excitatory synapses in a cell or group of cells. In one embodiment, the methods include contacting

the cells or group of cells with an antibody or antigen-binding fragment of this invention under conditions sufficient to detect the excitatory synapses in the cells or group of cells. In a specific embodiment, the antibody or antigen-binding fragment is detectably-labeled or is capable of producing a detectable label. Illustrative of such labels include a radionuclide; a protein tag; a chromophore; a fluorescent, chemiluminescent or phosphorescent molecule. In another specific embodiment the antibody or antigen-binding fragment thereof is labeled with at least one enzyme capable of producing a chromophore, a fluorescent, chemiluminescent or phosphorescent molecule.

In another aspect, the present invention provides a library that includes a plurality of the polynucleotides or the polypeptides of this invention including fragments or derivatives of those polynucleotides or polypeptides. Illustrative of such libraries include cDNA and genomic DNA libraries, combinatorial and peptide expression libraries.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1E are drawings showing the nucleotide sequence of SYNAP-a coding (SEQ ID NO. 1) and non-coding ~~(SEQ ID NO:2)~~ strands. The predicted amino acid sequence is also shown ~~(SEQ ID. NO. 3)~~.

Figures 2A-2E are drawings showing the nucleotide sequence of SYNGAP-b coding (SEQ ID NO. 4) and non-coding ~~(SEQ ID NO. 5)~~ strands. The predicted amino acid sequence is also shown (SEQ ID. NO. 6).

Figures 3A-3E are drawings illustrating the nucleotide sequence of SYNGAP-c coding (SEQ ID NO. 7) and non-coding (~~SEQ ID NO. 8~~) strands. Also shown is the amino acid sequence ~~(SEQ ID NO. 9)~~ and an untranslated amino acid sequence ~~(SEQ ID NO. 8A)~~ following the C-terminus of the predicted SYNGAP-c protein.

Figure 4A is a drawing showing the predicted amino acid sequence of SYNGAP-c (SEQ ID NO. 9).

Figure 4B is a schematic drawing showing the domain organization of SYNGAP-c.

Figure 4C is a drawing showing a sequence alignment between the Ras-GAP domain of SYNGAP-c (SEQ ID NO. 10), *Rattus norvegicus* (rn) Ras-GAP (L13151; SEQ ID NO. 11) and *Homo sapiens* neurofibromin (hs 1NF1, M38107; SEQ ID NO. 12). Identical residues are in bold type. Hyphens designate conceptual amino acid sequence deletions to maximize alignment.

Figure 5 is a drawing showing a sequence alignment between the pleckstrin homology (PH) of SYNGAP-a (SEQ ID NO. 13), *Homo sapiens* p120 RasGAP (Hs p120 Genbank Accession No. P20936; SEQ ID NO. 14); *D. melanogaster* GAP1 (Dm GAP1 Genbank Accession No. P48423); and Homo sapiens pleckstrin (Hs Plec Genbank Accession No. P08567). Dots designate conceptual amino acid sequence deletions to maximize alignment.

Figure 6 is a drawing showing a sequence alignment between the C2 domain of SYNGAP-a (SEQ ID NO. 17); *Homo sapiens* p120 RasGAP (Hs p120 Genbank Accession No. P20936; SEQ ID NO. 18); *Rattus norvegicus* Synaptotagamin II (Genbank Accession No. P29101; SEQ ID NO. 19); and *Bos taurus* Rabphilin 3A (Genbank Accession No. A48097; SEQ ID NO. 20). Dots designate conceptual amino acid sequence deletions to maximize alignment.

Figure 7A is a representation of a Northern blot showing high level of SYNGAP mRNA expression in the brain.

Figure 7B is a representation of a Western blot showing SYNGAP in rat tissues using immunoblot techniques. These antibodies recognized a 130kDa protein in HEK293T cells transfected with the SYNGAP cDNA (Lane 2) and in rat brain

homogenates (Lane 3). The 130kDa protein was not detected in mock transfected HEK293T cells (lane 1) and immunorecognition of the 130kDa protein in brain was blocked by preabsorbtion of the antibody with the antigen (Lane 4).

Figure 7C is a representation of a Western blot showing SYNGAP in rat tissues using the SYNGAP antibody. Expression of the SYNGAP protein is brain specific.

Figure 7D is a representation of an immunoblot showing that rat brain cortex crude homogenates (cortex) and cytosolic and membrane fractions include membrane-associated SYNGAP. Cortical membranes were extracted with the indicated detergents and then separated into soluble (S) and pellet fractions (P) and the distribution of SYNGAP detected using immunoblot techniques. SYNGAP is resistant to membrane extraction with non-denaturing detergents similar to other proteins located in the PSD fraction.

Figure 8 is a representation of an immunoblot illustrating that SYNGAP is associated with the ONEIDA receptor complex. In this figure, immunoprecipitates were analyzed for the presence of SYNGAP, NMDAR1, PSD-95 and GluR1.

Figures 9A-9F are representations of photomicrographs showing that SYNGAP is localized to synapses.

Figures 10A-10I are representations of photomicrographs showing that SYNGAP is specifically localized to excitatory synapses.

Figure 11 is a graph showing that the GAP domain of SYNGAP stimulates H-Ras GTPase activity.

DETAILED DESCRIPTION OF THE INVENTION

As summarized above, the present invention features molecules that relate to mammalian SYNGAP and methods of using such molecules. Particularly provided are novel polynucleotides and polypeptides that can be used in the methods. Further provided are methods for isolating the molecules and using same to treat or prevent disorders relating to SYNGAP. Additionally provided are screening methods that can be employed to detect compounds with capacity to diagnose or treat disorders associated with SYNGAP.

In general, optimal practice of the present invention can be achieved by use of recognized manipulations such as those involving molecular, cell culture, biochemical and electrophysiological techniques. For example, techniques for and purifying nucleic acids, methods for making and screening cDNA libraries, methods for making recombinant vectors, cleaving DNA with restriction enzymes, ligating DNA, introducing DNA into host cells by stable or transient means, culturing the host cells, methods for isolating and purifying polypeptides, methods for making antibodies, methods for assaying signal transduction molecules, methods for detecting protein binding and particularly binding to PDZ and receptor domains, computer-assisted methods for detecting nucleic acid or amino acid sequence homologies, and electrophysiological techniques are generally known in the field. See generally Sambrook et al., *Molecular Cloning* (2d ed. 1989); Ausubel et al., *Current Protocols in Molecular Biology*, (1989) John Wiley & Sons, New York; S. Altschul et al. *Nuc. Acids Res.*, 25: 3389-3402 (1997); Marshall, C.J. Current Opin. in Cell Biol. (1996) 8: 197; Sheng, M. Neuron (1996) 17: 575 and references cited therein.

Unless otherwise indicated, reference to SYNGAP means a polynucleotide or amino acid sequence that is substantially homologous to at least one of SYNGAP-a, SYNGAP-b, or SYNGAP-c. Preferred use of the term SYNGAP means SYNGAP-a, SYNGAP-b or SYNGAP-c. As noted, SYNGAP-a , SYGAP-b, and SYNGAP-c are alternatively spliced variants. Sometimes SYNGAP-c will be specifically referred to herein as "GAPSYN".

Polynucleotides of this invention can be derived from a variety of sources such as a mammalian source and particularly a rodent or a primate source, e.g., rat, rabbit, mouse or human source. It will be appreciated that the present disclosure provides ample information to facilitate isolation of a variety of mammalian SYNGAPs through use of recognized molecular techniques such as the Polymerase Chain Reaction (PCR) amplification and related amplification techniques. Typically, the isolated polynucleotide will be positioned in a recombinant vector, although in some cases it may be desirable to provide the polynucleotide without a recombinant vector, e.g., as a PCR-amplified product. Particularly, the polynucleotide can be provided in a suitable DNA vector capable for expressing an encoded SYNGAP or a fragment or derivative thereof in a eukaryotic or prokaryotic cell expression system. The polynucleotide may include operably linked transcriptional elements such as a promoter, leader and optimal enhancer sequences to drive expression of the encoded polypeptide in a desired host cell expression system. Alternatively, the DNA vector itself may provide some or all of the control elements. In general, polynucleotides of the invention that encode SYNGAP including fragments and derivatives thereof, are often made so that naturally-occuring SYNGAP control sequences (e.g., genomic control sequences) are reduced in number and preferably removed.

As will be apparant from the preceeding discussion, the ability to detect and modulate SYNGAP *in vitro* and *in vivo* is very important. For example, inappropriate SYNGAP activity may negatively impact synaptic function, signal transduction or both. That inappropriate SYNGAP activity may arise from one or a combination of different causes such as a genetic deficiency, chronic illness, viral infection, bacterial infection, trauma (e.g., emotional or physical) and the like. In particular, relationship between synapse function, receptor function and signal transduction may be adversely affected by the inappropriate SYNGAP activity. Thus, the present methods are particularly useful for diagnosing and treating disorders arising from unsuitable SYNGAP activity.

By the term "SYNGAP activity" or like term is meant those functions attributed to SYNGAP as discussed herein, e.g, PDZ domain and rasGTPase inhibition. It will be appreciated that related activities can impact SYNGAP activity including synthesis of SYNGAP (transcription and translation), SYNGAP processing (e.g., protein maturation including modification such as glycosylation), protein stability in SYNGAP-expressing cells, and neuromodulation.

As discussed above, the present invention provides methods to detect mammalian SYNGAP *in vitro* or *in vivo*. Further provided are useful methods for modulating, including enhancing, expression or activity of SYNGAP in particular cells such as those that include chemical synapses with SYNGAP. By way of illustration, one can provide an anti-sense SYNGAP molecule to neurons to selectively inhibit SYNGAP activity in those neurons. In addition, a suitable SYNGAP antibody or antigen-binding fragment thereof can be provided to reduce or eliminate SYNGAP function. Further, compounds identified by the methods of this invention can be administered *in vitro* or *in vivo* e.g., to enhance SYNGAP function including increasing the number or quality of chemical synapses that include SYNGAP.

In general, therapuetic methods of this invention include administration of a therapeutically effective amount of a SYNGAP or SYNGAP-related molecule to a subject and particularly a human patient in need of such treatment. Therapuetic methods of the invention also include administration of an effective amount of compound identified by this invention to the subject, in need of such treatment for an indication as disclosed herein.

Illustrative subjects for the purposes of this invention include those mammals suffering from or susceptible to those conditions generally discussed above, ie. disorders of the CNS and PNS such as an affective disorder, cognitive disorder, or a neurodegenerative disorder. In particular, a wide variety of CNS disorders may be alleviated by selectively enhancing or inhibiting SYNGAP activity in the CNS and

particularly in the brain. As will be shown below, SYNGAP is predominantly expressed in the brain. Illustrative CNS disorders are affective disorders (e.g., depression), disorders of thought (e.g., schizophrenia) and degenerative disorders, as well as disorders manifested by application of anesthesia. CNS disorders of severe impact include pre-senile dementia (sometimes referred to as Alzheimer's disease (AD) or early-onset Alzheimer's disease), senile dementia (dementia of the Alzheimer's type), Parkinson's disease (PD), and Huntington's disease (HD, sometimes referenced as Huntington's chorea). Such CNS disorders are well-represented in the human population. See generally; Gusella, J.F. et al. (1983) *Nature* 306: 234; Borlauer. W. and Jprmuloewoca. P. (eds.) (1976*); Adv. in Parkinsonism: Biochemistry, Physiology, Treatment. Fifth International Symposium on Parkinson's Disease* (Vienna) Basel: Roche; and references cited therein. Subjects that have suffered acute CNS trauma also may be treated in accordance with the invention, e.g. brain or spinal cord ischemia or trauma, stroke, heart attack or neorological deficits that may be associated with surgery.

In the methods of the invention, a desired therapuetic molecule (ie. a suitable SYNGAP or SYNGAP-related molecule or identified compound) can be administered to a subject in need of treatment or suspected of needing treatment in any of several ways. For example, a desired SYNGAP or SYNGAP-related polynucleotide, immune system molecule or a therapuetic compound can be administered as a prophylactic to prevent the onset of or reduce the severity of a targeted condition. Alternatively, the therapuetic molecule can be administered during or following the course of a targeted condition.

More specifically, the therapuetic molecule can be administered to a subject, either alone or in combination with one or more therapeutic agents, as a pharmaceutical composition in mixture with conventional excipient, i.e. pharmaceutically acceptable organic or inorganic carrier substances suitable for parenteral, enteral or intranasal application which do not deleteriously react with the active compounds and are not deleterious to the recipient thereof. Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions, alcohol, vegetable oils, polyethylene glycols,

gelatin, lactose, amylose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid monoglycerides and diglycerides, petroethral fatty acid esters, hydroxymethyl-cellulose, polyvinylpyrrolidone, etc. The pharmaceutical preparations can be sterilized and if desired mixed with auxiliary agents, e.g., lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, colorings, flavorings and/or aromatic substances and the like which do not deleteriously react with the active compounds.

Such compositions may be prepared for use in parenteral administration, particularly in the form of liquid solutions or suspensions; for oral administration, particularly in the form of tablets or capsules; intranasally, particularly in the form of powders, nasal drops, or aerosols; vaginally; topically e.g. in the form of a cream; rectally e.g. as a suppository; etc.

The pharmaceutical agents may be conveniently administered in unit dosage form and may be prepared by any of the methods well known in the pharmaceutical arts, e.g., as described in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., Easton, PA, 1980). Formulations for parenteral administration may contain as common excipients such as sterile water or saline, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, hydrogenated naphthalenes and the like. In particular, biocompatible, biodegradable lactide polymer, lactide/glycolide copolymer, or polyoxyethylene-polyoxypropylene copolymers may be useful excipients to control the release of certain of the compounds.

Other potentially useful parenteral delivery systems include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation administration contain as excipients, for example, lactose, or may be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate and deoxycholate, or oily solutions for administration in the form of nasal drops, or as a gel to be applied intranasally. Formulations for parenteral administration

may also include glycocholate for buccal administration, methoxysalicylate for rectal administration, or citric acid for vaginal administration. Other delivery systems will administer the therapeutic agent(s) directly, e.g., by use of stents.

A therapuetic molecule of this invention can be employed in the present treatment methods as the sole active pharmaceutical agent or can be used in combination with other active ingredients, e.g., those compounds known in the field to be useful in the treatment of cognitive and neurological disorders.

The concentration of one or more treatment compounds in a therapeutic composition will vary depending upon a number of factors, including the dosage of the therapuetic compound to be administered, the chemical characteristics (e.g., hydrophobicity) of the composition employed, and the intended mode and route of administration. In general terms, one or more than one of the therapuetic compounds compounds may be provided in an aqueous physiological buffer solution containing about 0.1 to 10% w/v of a compound for parenteral administration. As noted above, GAPYSN antibodies and antigen-binding fragments thereof can be modifed according to standard methods to deliver useful molecules or can be modified to include detectable labels and tags to facilitate visualization of synapses including SYNGAP.

It will be appreciated that the actual preferred amounts of active compounds used in a given therapy will vary according to e.g. the specific compound being utilized, the particular composition formulated, the mode of administration and characteristics of the subject, e.g. the species, sex, weight, general health and age of the subject. Optimal administration rates for a given protocol of administration can be readily ascertained by those skilled in the art using conventional dosage determination tests conducted with regard to the foregoing guidelines. Suitable dose ranges may include from about 1μg/kg to about 100mg/kg of body weight per day.

Therapuetic compounds identified by the present methods can be suitably administrated by conventional routes. For example, when the therapuetic compound is a synthetic or naturally-occuring chemical compound such as a drug, it will be preferred to administer the compound in a protonated and water-soluble form, e.g., as a pharmaceutically acceptable salt, typically an acid addition salt such as an inorganic acid addition salt, e.g., a hydrochloride, sulfate, or phosphate salt, or as an organic acid addition salt such as an acetate, maleate, fumarate, tartrate, or citrate salt. Pharmaceutically acceptable salts of therapeutic compounds of the invention also can include metal salts, particularly alkali metal salts such as a sodium salt or potassium salt; alkaline earth metal salts such as a magnesium or calcium salt; ammonium salts such an ammonium or tetramethyl ammonium salt; or an amino acid addition salts such as a lysine, glycine, or phenylalanine salt.

Current therapuetic practice typically utilizes one or a combination of different drugs to treat the disorders described above. As noted, the present invention provides methods for detecting compounds capable of treating or preventing the disorders. Compounds identified by these methods may be used either alone, or in combination with currently used therapies to alleviate the disorders or to reduce symptoms associated with the disorders. In particular, specific drugs that have been reported to be of use in the treatment of affective disorders, e.g., depression, manic-depressive disorders, anxiety disorders such as panic attacks and the like. Many of these drugs have been reported to work by modulating synaptic function, e.g., by altering receptor activity. According to methods of the present invention, compounds with capacity to modulate neuroreceptors, e.g., by increasing SYNGAP activity, may be similarly effective at treating depressive disorders. Such compounds may be identified by practice of the screening methods described herein.

Compounds identified by the methods of the invention can be further tested if desired in standard assays used to measure higher nervous system functions such as habituation, sensitization, learning and memory. Examples of such systems include those

using well known test organisms such as *Aplysia*, *C. elegans*, *D melanogaster*, primates such as monkeys, and rodents such as mice, rabbits and rats. Preferred compounds are those that can increase or decrease at least one of these functions by at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% up to about 100% as determined by a suitable testing protocol recognized in the test organism selected.

Compounds identified by the present methods can be administered to a subject and preferably a human patient suffering from or suspected of suffering from a SYNGAP-related disorder as described above.

Particularly preferred systems for performing the testing methods of this invention involve cell culture assays and especially cell culture assays employing primary or cultured cells dervived from the nervous system. Preferred cultured cells are capable of expressing or express excitatory chemical synapses including SYNGAP such as CNS-derived cells such as those derived from the brain. Illustrative cells include are provided below in the examples. If desired, a cultured cell line can be tested for SYNGAP expression by determining if the cells express or can be made to express SYNGAP. Methods for detecting expression include immunological methods involving a suitable SYNGAP antibody, e.g., a Western blot, RIA, ELISA or other immunoassay.

In addition to the specific CNS- and PNS-related applications described herein, the present invention can also be used to therapeutically intervene in other systems that are affected by inappropriate SYNGAP activity. Such systems include the endocrine system for treatment of hormonal imbalances, the immune system for intervention in antigen processing, secreted immunomodulators, and viral processing, as well as anti-tumor applications, such as regulation of synapse formation in malignancies of the neuroendocrine system. To reduce or avoid CNS-or PNS-related side-effects, compounds identified in the methods of this invention may be re-screened multiple times, e.g., 2, 3, 4, or 5 times to identify compounds that specifically modulate SYNGAP in the neurons.

As discussed, the present invention provides isolated polynucleotides that encode SYNGAP or a fragment or a derivative of SYNGAP. The isolated polynucleotides may be cloned or subcloned using nearly any method known in the art. See e.g., Sambrook, J. et al., *supra*. In particular, nucleotide sequences of the invention may be cloned into any of a large variety of vectors. Possible vectors include, but are not limited to, cosmids, plasmids or modified viruses, although the vector system must be compatible with the host cell used. Viral vectors include, but are not limited to, lambda, simian virus, bovine papillomavirus, Epstein-Barr virus, and vaccinia virus. Viral vectors also include retroviral vectors, such as Amphatrophic Murine Retrovirus (see Miller et al., *Biotechniques*, 7:980-990 (1984)), incorporated herein by reference). Plasmids include, but are not limited to, pBR, pCMV5, PUC, pGEM (Promega), and Bluescript™ (Stratagene) plasmid derivatives. Introduction into and expression in host cells is done for example by, transformation, transfection, infection, electroporation, etc. See the examples which follow for particularly preferred recombinant vectors.

For preferred production of anti-sense RNA, use of specified recombinant vectors typically including strong bacterial or eukaryotic (e.g., viral) promoters will usually be desired. See e.g., Ausubel et al. *supra*.

The term "vector" or "recombinant vector" as used herein means any nucleic acid sequence of interest capable of being incorporated into a host cell and resulting in the expression of a nucleic acid sequence of interest. Vectors can include, e.g., linear nucleic acid sequences, plasmids, cosmids, phagemids, and extrachromosomal DNA. Specifically, the vector can be a recombinant DNA. Also used herein, the term "expression" or "gene expression", is meant to refer to the production of the protein product of the nucleic acid sequence of interest, including transcription of the DNA and translation of the RNA transcript. Most recombinant vectors will include a "cloning site" which as used herein is intended to encompass at least one restriction endonuclease site. Typically, multiple different restriction endonuclease sites (e.g., a polylinker) are contained within the vector to facilitate cloning.

As noted, preferred polynucleotides of this invention encode a mammalian SYNGAP having a molecular of between about 100, 110, 120, 130, 140, or about 150 kDA or greater. Also preferred are those polynucleotides that are at least 70%, 75%, 80%, 90%, 95%, 99% or greater sequence identity to any of the nucleotide sequences specifically shown in SEQ ID NOS: ~~1-2, 4-5, or 7-8~~. As will be fully appreciated, such sequences are substantially homologous to the sequences shown in SEQ ID NOS: ~~1, 2, 4-5, or 7-8~~. A more preferred polynucleotide of the invention encodes the rat SYNGAP shown in SEQ ID NOS. ~~3, 6 or 9~~. A specifically preferred polynucleotide encodes the rat SYNGAP shown in SEQ ID NO. ~~9~~. See Figures 1A-1E; 2A-2E; and 3A-3E.

By the term "substantially homologous" is meant relationship between two nucleic acid molecules and generally refers to subunit sequence similarity between the two molecules. Typically, the two nucleic acid molecules will be DNA. When a subunit position in both of the DNA molecules is occupied by the same monomeric subunit, i.e. a nucleotide, then they are homologous at that position. Homology between the two sequences is a direct function of the number of matching or homologous positions, e.g., if 50% of the subunit positions in the two DNA sequences are homologous then the two sequences are 50% homologous. By "substantially homologous" is meant largely but not wholly homologous. More particularly, the term is meant to denote at least about 70% or greater homology as defined above with respect to the rat SYNGAP sequences illustrated in SEQ ID NOs: ~~1-2, 4-5, or 7-8~~. Preferred nucleotide sequences of the invention have at least about 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% homology as defined above with respect to the rat SYNGAP sequences illustrated in SEQ ID NOs: ~~1-2, 4-5, or 7-8~~.

The term "substantially homologous" is also used herein with reference to relationship between two polypeptide sequences and generally refers to subunit sequence similarity between the two molecules. When a subunit position in both of the polypeptides is occupied by the same monomeric subunit, i.e. an amino acid sometimes refered to as an amino acid residue, then they are homologous at that position. Homology

between the two sequences is a direct function of the number of matching or homologous positions, eg., if 50% of the subunit positions in the two polypeptides are homologous then the two sequences are 50% homologous. By "substantially homologous" is meant largely but not wholly homologous. More particularly, the term is meant to denote at least about 70% or greater homology as defined above with respect to the rat SYNGAP sequences illustrated in SEQ ID NO: ~~3, 6, or 9.~~ 2, 4 or 6 Preferred polypeptides of the invention have at least about 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% homology as defined above with respect to the rat SYNGAP sequences illustrated in SEQ ID NO: ~~3, 6, or 9~~. 2, 4 or 6

Two substantially homologous polynucleotides can be identified by one or a combination of different strategies. For example, in one approach, a polynucleotide of this invention that is substantially homologous to any one of sequences shown in SEQ ID NOs: ~~1-2, 4-5, or 7-8~~ 1, 3 or 5 in addition to fragments and derivatives thereof of a length sufficient to bind to the sequences in the sequences, can be identified by employing moderately stringent conditions. In particular, moderate stringency conditions are meant to include a hybridization buffer comprising about 20% formamide in 0.8M saline/0.08M sodium citrate (SSC) buffer at a temperature of 37°C and remaining bound when subject to washing once with that SSC buffer at 37°C. Additionally, highly stringent conditions are meant to include a hybridization buffer comprising about 50% formamide in SSC buffer at about 42 °C and remaining bound when washed in SSC buffer. See e.g., Sambrook et al. *supra*.

Additional methods of detecting and quantitating substantial homology refer to so-called "dry" methods and include use of publically available computer programs that can readily determine homology between nucleic acids of known or partially known sequence. Exemplary of such programs include the BLAST program available from the National Library of Medicine (Genbank). See also S. Altschul et al. *J. Mol. Biol.*, 215:403-410 (1990); and S. Altschul et al. *Nuc. Acids Res.*, 25: 3389-3402 (1997) for specific disclosure relating to use of the BLAST program.

Nucleic acid fragments and derivatives of this invention preferably should comprise at least about 12 to about 50 nucleotides, at least about 60, 100 to 200 nucleotides, at least about 300, 400, to about 500 nucleotides, or at least about 1000, 1500, 2000, 2500, 3000, 3500 to about 4000 nucleotides or more. In some preferred embodiments, the nucleic acid fragment or derivative is bound to a suitable moiety, sometimes called a tag, which permits ready identification such as a radionucleotide, fluorescent or other chemical identifier.

The polynucleotide sequences of the invention can be altered by mutations such as substitutions, additions or deletions (contiguous or non-contiguous) that can provide for substantially homologous nucleic acid sequences. In particular, a given nucleotide sequence can be mutated *in vitro* or *in vivo*, to create variations in the nucleotides, e.g., to form new or additional restriction endonuclease sites or to destroy preexisting ones and thereby to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used including, but not limited to, *in vitro* site-directed mutagenesis (Hutchinson et al., *J. Biol. Chem.*, 253:6551 (1978)), use of TAB Registered TM linkers (Pharmacia), PCR-directed mutagenesis, and the like.

It will be appreciated that due to the degeneracy of genetic code , a number of different nucleic acid sequences may be used in the practice of the present invention. This includes the substitution of different codons encoding the same amino acid residue within the sequence, thus producing a silent or nearly silent change. Almost every amino acid except tryptophan and methionine is represented by several codons. Often the base in the third position of a codon is not significant, because those amino acids having 4 different codons differ only in the third base. This feature, together with a tendency for similar amino acids to be represented by related codons, increases the probability that a single, random base change will result in no amino acid substitution or in one involving an amino acid of similar character. See generally Alberts et al., *Molecular Biology of the Cell,* (1989) Garland Publishing, New York.

Thus, the present invention includes polynucleotides with genetic alterations that do not substantially impact SYNGAP function as related herein. The genetic alterations can be synthetic, i.e., can be introduced experimentally, or may be naturally-occurring, e.g., in the form of SYNGAP isoforms or allelic variants. Additionally, SYNGAP-a, SYNGAP-b, and SYNGAP-c are illustrative of naturlly-occuring splice variants. See Figures 1A-1E; 2A-2E; and 3A-3E.

As noted, the present invention provides oligonucleotide primers that are complementary to any of the nucleotide sequences shown in SEQ ID NOs: ~~1-2, 4-5, or 7~~ 1, 3, or 5 ~~&~~. In most cases, the primers will be a DNA sequence of between about 12 to about 70 nucleotides in length preferably about 20, 30, 40, to about 50 or about 55 nucleotides in length. The oligonucleotide primers can suitably include restriction sites to add specific restriction enzyme cleavage sites to the PCR product as needed, e.g., to introduce a ligation site. Preferred DNA oligonucleotide primers are spaced from one another in opposing direction relative to extension of the primers. That is, the primers are spaced relative to each other on a polynucleotide template (usually on different strands) sufficient to produce an amplification product of at least about 50 nucleotides, at least about 60 to about 100 nucleotides, at least about 200 to 500 nucleotides, at least about 600 to 1000 nucleotides, or at least about 1000 to 3000 nucleotides up to about 4000 nucleotides as determined, e.g., by gel electrophoresis. Synthetic methods for making oligonucleotide primers are well known in the field. Exemplary primers are provided in the examples which follow.

Preferred polynucleotides of this invention are capable of modulating and preferably inhibiting Ras by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, up to about 100% in what has been referred to as a standard Ras GTPase assay. A variety of Ras GTPase assays are known in the field. For example, a preferred standard assay includes at least one of the following general steps:

a) mixing Ras or a GTPase- active portion of Ras with a suitable amount of detectably-labeled GTP (e.g., γ^{32}P-GTP],

c) contacting the mixture with a mammalian SYNGAP, e.g., the amino acid sequence shown in SEQ ID NO: 1 2 or a fragment thereof including at least a Ras-GTPase active portion of the SYNGAP (ie., the GAP domain); and

d) detecting binding of the detectably-labeled GTP to the Ras or Ras portion.

As will be shown below, the Ras and/or the SYNGAP protein can be fused (ie. covalently linked) to a suitable protein tag such as GST to facilitate protein isolation and purification. If desired, the above general method can be adapted to include a suitable control which can be a GST-fusion protein such as those known in the field. In general, the control is prepared and incubated under the same or closely related conditions as the assay but does not include addition of the SYNGAP or fragment thereof. A particularly preferred method for detecting Ras-GTPase activity involves measuring γ^{32}P-GTP over a time period of between from about 30 seconds to about one hour or longer, typically from about 1 minute to about 20 minutes or longer. See Settleman et al. (1992) *Cell.* 69:539.

By the term "Ras-GTPase" portion of SYNGAP is meant at least the SYNGAP Ras-GTPase domain which domain is capable of negatively regulating Ras as determined by the standard Ras-GTPase assay described herein. Additional SYNGAP Ras-GTPase domains are those domains that are substantially homologous to the GAP domain shown between amino acid residues 266 and 502 of the rat SYNGAP sequence. See Figure 4C and SEQ ID No. 11. Preferred Ras-GTPase portions have a length of between about 200, 300 to about 400 amino acids and include amino acid residues (bold) shown in 4C (GAPSYN). The bolded amino acids shown in Figure 4C will typically be present in the Ras-GTPase portion in the alignment shown.

By the term "pleckstrin homology" (PH) is meant an amino acid sequence that is substantially homologous to any one of the following amino acid sequences: SynGAP-a, 162 to 243; SYNGAP-b, 60-141; and SYNGAP-c, 4 to 85. See Figures 1A-1E; 2A-2E; and 3A-3E; and 4A-B. Preferred PH domains have a length of between about 20, 30, 40, 50, 60, 70, 80, 90, to about 100 amino acids and include amino acid residues (bold)

shown in Figure 5 (SYNGAP-a). The bolded amino acids shown in Figure 5 will typically be present in the PH domain in the alignment shown.

By the term "C2 domain" is meant an amino acid sequence that is capable of modulating phospholipid-dependent calcium (Ca^{+2}) binding to the SYNGAP as determined by assays disclosed herein. Preferred are those sequences which are substantially homologous to any one of the following amino acid sequences: SynGAP-a, 245 to 354; SYNGAP-b, 143 to 252; and SYNGAP-c, 87 to 196. See Figures 1A-1E; 2A-2E; 3A-3E and 4A-B. Additionally preferred C2 domains have a length of between about 90, 100, 120, 130, up to about 150 and include amino acid residues (bold) shown in Figure 6 (SYNGAP-a). The bolded amino acids shown in Figure 6 will typically be present in the PH domain in the alignment shown.

A variety of phospholipase C assays are known in the field which assays can be readily adapted in accord with the present invention. See e.g., James, S.R. et al., (1997) *Cell Signal.* 329; and Hurley, J.H. (1997) *Curr. Opin. Struct. Biol.* 7:557; and references cited therein.

The RasGTPase activating activity of SYNGAP can be measured by a variety of means including use of the MAP kinase cascade as a reporter in a primary or immortalized cell culture, e.g., hippocampal neurons or HEK 293, NIH3T3 cells. The regulation of Ras activity by SYNGAP in a selected cell or cell line can be observed by transfecting the cells with a SYNGAP cDNA plasmid with, e.g., a luciferase or other suitable reporter construct that is activated by the MAP kinase cascade. See e.g., 1997 instruction manual entitled *PathDetect™ In Vivo Signal Transduction Pathway Trans-Reporting Systems*, pp.1-20 (Stratagene Cloning Systems, La Jolla, Ca). Alternatively, SYNGAP cDNA can be transfected into primary culture cells with the reporter construct. SYNGAP activity can then be indirectly assayed by quantifying luciferase (or other reporter activity) with a luminometer or other suitable measuring device. Various agents, e.g., drugs, that regulate SYNGAP activity of the pathway can be rapidly screened by this

method. For example, a variety of drugs such as growth factors, cytokines, neurotransmitters and the like can be tested for capacity to regulate SYNGAP. Importantly, agents that activate or inhibit SYNGAP activity can be rapidly analyzed.

Additionally preferred polynucleotides of this invention encode a mammalian SYNGAP or SYNGAP-related amino acid sequence that is capable of binding 1, 2, 3, up to about 10 PDZ domains as determined by a standard PDZ domain binding assay. For example, a prefered standard PDZ domain binding assay involves what has been referred to as the yeast two-hybrid system.

In general, the yeast GAL4 two hybrid system can detect protein-protein interactions based on the reconstitution of function of GAL4 (yeast transcriptional activator) by activation of a GAL1-lacZ reporter gene. Like several many other transcription activating factors, the GAL4 protein contains two distinct domains, a DNA binding domain and a transcription activation domain. Each domain can be independently expressed as a portion of a fusion protein composed of the domain, and a second, "bait" interacting protein. The two fusion proteins are then independently expressed together in a cell. When the two GAL4 domains are brought together by a binding interaction between the two "interacting" proteins, transcription of a reporter gene under the transcriptional control of GAL4 is initiated. The reporter gene typically has a promoter containing GAL4 protein binding sites (GAL upstream activating sequences, UAS[G]). Several examples of yeast two-hybrid assays have been reported. See e.g., U.S. Pat. Nos. 5,693,476 and 5,695,941.

A two hybrid system such as is described above may be used to identify proteins and particularly synaptic proteins that include at least one suitable SYNGAP-binding PDZ domain. As noted above and more specifically in the following discussion, that interaction is believed to occur due to binding between the PDZ domain and the C-terminal sequence ((Tor S), X V) at the end of SYNGAP wherein X is any of the 20 common amino acids (Ala, Arg, Asn, Asp, Lys, Gln, Glu, Gly, His, Ile, Lev, lys, Met,

Phe, Pro, Ser, Thr, Trp, Tyr, Val). A specific PDZ binding assay involves at least one of the following steps:

a) fusing a polynucleotide encoding SYNGAP or a suitable fragment thereof to the GAL4 DNA binding domain (G4BD) (fusion protein) in a suitable yeast expression vector,

b) transforming the vector carrying fusion protein into yeast cells harboring a suitable reporter gene activated by GAL4 (e.g., a suitable LacZ construct),

c) transforming the cells with a second vector carrying a fusion between a polypeptide comprising at least one PDZ domain (e.g, PSD-95/SAP90) and the transcription activating domain of yeast GAL4; and

d) screening the transformants for expression of the reporter gene in the yeast.

In most cases, the yeast transformants are screened using a beta -galactosidase (beta -gal) assay on plates containing the chromogenic substrate X-gal. Reporter-expressing cells can be selected, cloned, and analyzed if desired. It may be of interest in some instances to use a second two hybrid system, described in detail in Ausubel, et al., that utilizes a native E. coli LexA repressor protein. That protein binds tightly to appropriate operators. A plasmid is used to express one of a pair of interacting proteins (the "bait" protein) as a fusion to LexA. Example 2 below descibes an especially preferred assay for detecting PDZ binding to SYNGAP using a yeast two-hybrid system.

Preferred polynucleotides are capable of encoding sequence that result in at least about a 10% to 20% up to about a 100% increase or more of positive (blue) colonies relative to a suitable control. Colony number can be determined by inspection.

Additional standard assays can be conducted to detect PDZ binding to SYNGAP and SYNGAP- related polypeptide s of this invention. For example, specific biochemical assays are useful for detecting PDZ interactions including certain partner assays. For example, a polynucleotide can be expressed and the encoded polypeptide immobilized on a suitable solid support. A suitable PDZ protein such as PSD-95/SAP90 or a fragment or

a derivative thereof is contacted to the solid support under conditions conducive to binding between the PDZ protein and the SYNGAP or SYNGAP-related polypeptide . Typically, the PDZ protein will be detectably-labeled, e.g., with a radionuclide or other suitably detectable tag to facilitate detection and quantitation, if desired, of the binding. Preferred methods for detecting the binding include well known panning methods, e.g., immunopanning, preferably conducted in multi-well plates. Alternatively, the binding can be assayed by conventional immunological techniques such as RIA, ELISA, affinity chromatography, Western blots, etc. Preferred polynucleotides are capable of encoding polypeptides that exhibit and increase in binding to the PDZ protein of at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, up to 100% or more relative to a suitable control polypeptide that does not include a detectable PDZ domain (e.g, LacZ).

Additionally preferred polynucleotides of this invention are capable of encoding polypeptides that bind PDZ domains as detected by use of affinity biosensor methods. Such methods may be based on a variety of detectable effects including surface plasmon resonance (SPR). SPR is particular advantageous for monitoring molecular interactions in real-time, enabling a sensitive and comprehensive analysis of the effects of test compounds on the binding interactions between two proteins than the methods discussed above.. Preferred polynucleotides of this invention are capable of encoding polypeptides that are capable of binding proteins comprising at least one PDZ domain and causing a change in reflectance intensity of at least about 10% to about 20% relative to a suitable control protein (e.g., LacZ). See e.g., Cullen, D. C., et al., *Biosensors* 3:211-225 (1988).

The above-mentioned methods can be readily adapted to detect compounds that can modulate SYNGAP activity, e.g., by modulating SYNGAP binding to a polypeptide comprising one or more PDZ domains, modulating SYNGAP-mediated Ras GTPase activity, or both. In general, any of the methods can be optimized to include addition of one or more test compounds optionally in parallel with a suitable control, to detect modulation.

A variety of different compounds may be screened using methods of the present invention. They include peptides, macromolecules, small molecules, chemical and/or biological mixtures, and fungal, bacterial, or plant extracts. Such compounds, or molecules, may be either biological, synthetic organic, or even inorganic compounds, and may be obtained from a number of sources, including commercial or publically-accessible vendors of libraries of compounds.

In cases where an identified compound is a peptide, the peptide may be utilized to aid in the discovery of small molecule mimetics. Methods of the present invention are well suited for screening libraries of compounds in multi-well plates (e.g., 96-well plates), with a different test compound in each well. In particular, the methods may be employed with combinatorial libraries. A variety of combinatorial libraries of random-sequence oligonucleotides, polypeptides, or synthetic oligomers have been proposed including small-molecule libraries. Alternatively, the library may be formed by solid-phase synthetic methods in which beads containing different-sequence oligomers that form the library are alternately mixed and separated, with one of a selected number of subunits being added to each group of separated beads at each step. The identity of library compounds with desired effects on the binding of an SYNGAP and a protein comprising one or more PDZ domains such as PSD-95/SAP90 can be determined by any of the methods described herein. See e.g., Houghten, R. A., (1985) *PNAS (USA)* 85:5131.

As noted, particularly preferred polynucleotides of this invention exhibit a length of between about 50 to about 100 nucleotides, about 200, 300, 400, 500, 600, 800, 1000, 1500, 2000, 2500, 3000, 3500, 4000 or more as determined by standard nucleic acid sizing techniques such as agarose or polyacrylamide gel electrophoresis. The polynucleotide can be RNA, DNA or a chimera thereof as desired.

Exemplary host cells which can express the isolated polynucleotides of this invention are known in the field and include bacterial cells (e.g., *E. coli*) such as MM294,

DM52, XL1-blue (Stratagene) strains of *E. coli*, and animal cells (e.g., CV-1 and COS-7 cells). In addition, it is possible to express certain isolated nucleic acids of the invention in certain yeast cells (e.g., *S. cerevisiae*), amphibian cells (e.g., *Xenopus oocyte*), and insect cells (e.g., *Spodoptera frugiperda* and *Trichoplusia ni*). Methods for expressing isolated and recombinant DNA in these cells are known. See e.g., Sambrook et al., *Molecular Cloning* (2d ed. 1989), Ausubel et al. *supra*, and Summer and Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures:* Texas *Agricultural Experimental Station Bulletin* No. 1555, College Station Texas (1988). Specifically preferred host cells are discussed more fully below.

The polynucleotides of this invention can be readily made by techiques well known in the field including those techniques involving large-scale production thereof such as those including use of roller bottles, bioreactors and the like.

The term "complementary" or like term refers to the hybridization or base pairing between nucleotides or nucleic acids, such as, for instance, between the two strands of a double stranded DNA molecule or between an oligonucleotide primer and a primer binding site on a single stranded nucleic acid to be sequenced or amplified. Complementary nucleotides are, generally, A and T (or A and U), or C and G. Two single stranded RNA or DNA molecules are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared and with appropriate nucleotide insertions or deletions, pair with at least about 95% of the nucleotides of the other strand, usually at least about 98%, and more preferably from about 99 to about 100%. Complementary polynucleotide sequences can be identified by a variety of approaches including use of well-known computer algorithms and software.

Polynucleotides of this invention are typically isolated, meaning that the polynucleotides usually constitute at least about 0.5%, preferably at least about 2%, and more preferably at least about 5% by weight of total polynucleotide present in a given fraction. A partially pure polynucleotide constitutes at least about 10%, preferably at

least about 30%, and more preferably at least about 60% by weight of total nucleic acid present in a given fraction. A pure polynucleotide constitutes at least about 80%, preferably at least about 90%, and more preferably at least about 95% by weight of total polynucleotide present in a given fraction. Purity can be determined by standard methods including gel electrophoresis.

It is preferred that the polypeptides of the present invention be substantially pure. That is, the polypeptides have been isolated from cell substituents that naturally accompany it so that the polypeptides are present preferably in at least 80% or 90% to 95% homogeneity (w/w). Polypeptides having at least 98 to 99% homogeneity (w/w) are most preferred for many pharmaceutical, clinical and research applications. Once substantially purified the polypeptide should be substantially free of contaminants for therapeutic applications. Once purified partially or to substantial purity, the polypeptides can be used therapeutically, or in performing a desired assay. Substantial purity can be determined by a variety of standard techniques such as chromatography and gel electrophoresis.

Particularly preferred polynucleotides and polypeptides of this invention are provided as substantially sterile formulations.

As noted, illustrative polynucleotides of this invention include those encoding a mammalian SYNGAP as identified herein. Preferably the polynucleotides are at least substantially homologous to any of the sequences shown in SEQ ID NOs: 3, 4, or 6 ~~3, 6 or 9~~. For example, the mammalian SYNGAP can be derived from a primate such as a monkey or a human; or the mammalian SYNGAP can be derived from a rodent such as a rat, mouse, guinea pig, or rabbit. By the term "derived from" is meant that at least a portion of the polynucleotide was isolated from or copied from a naturally-occuring mammalian nucleic acid such as a genomic DNA or cDNA.

The SYNGAP and SYNGAP-related polypeptides of the present invention can be separated and purified by appropriate combination of known techniques. These methods include, for example, methods utilizing solubility such as salt precipitation and solvent precipitation, methods utilizing the difference in molecular weight such as dialysis, ultra-filtration, gel-filtration, and SDS-polyacrylamide gel electrophoresis, methods utilizing a difference in electrical charge such as ion-exchange column chromatography, methods utilizing specific affinity such as affinity chromatograph, methods utilizing a difference in hydrophobicity such as reverse-phase high performance liquid chromatograph and methods utilizing a difference in isoelectric point, such as isoelectric focusing electrophoresis, metal affinity columns such as Ni-NTA. See generally Sambrook et al. and Ausubel et al. *supra* for disclosure relating to these methods.

It is preferred that the polypeptides of this invention be substantially pure. That is, the fusion proteins have been isolated from cell substituents that naturally accompany it so that the fusion proteins are present preferably in at least 80% or 90% to 95% homogeneity (w/w). Fusion proteins having at least 98 to 99% homogeneity (w/w) are most preferred for many pharmaceutical, clinical and research applications. Once substantially purified the fusion protein should be substantially free of contaminants for therapeutic applications. Once purified partially or to substantial purity, the soluble fusion proteins can be used therapeutically, or in performing *in vitro* or *in vivo* assays as disclosed herein. Substantial purity can be determined by a variety of standard techniques such as chromatography and gel electrophoresis.

Preferred polypeptides of this invention generally exhibit a molecular weight from about 100, 110, 120, 130, 140, to about 150 kDa as determined by standard protein sizing manipulations such as polyacrylamide gel electrophoresis and centrifugation sedimentation. Additionally preferred are those polypeptides that are substantially homologous to the SYNGAP sequence shown in SEQ ID NO: 6 (ie. at least 70%, 80%, 90%, 95% up to about 99% homologous) as determined by the methods described earlier.

Particularly preferred are those polypeptides having from between about 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, up to about 1500 amino acids.

The term " amino acid sequence" as used herein generally refers to any polymer preferably consisting essentially of any of the 20 naturally occurring amino acids regardless of its size. Although the term "protein" is often used in reference to relatively large proteins, and "polypeptide" or "peptide" is often used in reference to small amino acid sequences, use of these terms in this field often overlaps. Thus, it will be understood that the term generally refers to proteins, polypeptides, and peptides unless otherwise noted.

As noted, the present invention provides a variety of methods for detecting a Ras-activated signaling pathway or a phospholipid-activated pathway (sometimes called a Ras-activated or a phospholipid-activated second messenger pathway, respectively). Additionally, the present methods provide means of detecting modulation of Ras-Raf (MAP kinase) cascades. In preferred embodiments the methods include a Ras- or inositol triphosphate response system which systems can be provided in a suitable host cell or cell lysate.

In general, the response systems can be obtained by coupling a mammalian SYNGAP or a suitable fragment thereof encoded by an isolated cDNA molecule to an appropriate second messenger response system. Particular SYNGAP fragments of interest include those that modulate Ras activity or include the C2 domain as disclosed herein. The system can include but is not limited to systems relating to adenylate cyclase, phosphoinositide hydrolysis, guanylate cylase, MAP kinase, and certain synaptic receptor proteins such as the NMDA receptor. One way to obtain a suitable response system is by transfection of an appropriate isolated polynucleotide of this invention into a suitable host cell that includes the desired second messenger system. Alternatively, a lysate can be prepared from the cell that includes purified or partially purifed molecules in the pathway. When cells are used, the cells can be obtained from pre-existing cell lines or

can be generated by inserting suitable components of the desired second messenger system into those existing cell lines. Such a transfection system will preferably provide, in a single cell line, a complete Ras- or inositol triphosphate response system for detection of componds capable of modulating the desired signalin pathway.

As noted, the present also embraces immune system molecules and particularly antibodies and antigen-binding fragments thereof that binding mammalian SYNGAP and particularly the SYNGAP sequence shown in SEQ ID NO: 2.

In particular, antibodies of the invention can be prepared by techniques generally known in the art, and are typically generated to a purified sample of SYNGAP, SYNGAP-related polypeptide. The antibodies also can be generated from an immunogenic peptide that comprises one or more epitopes of SYNGAP. Examples of such immunogenic peptides are described more fully below in the examples. As discussed above, monoclonal antibodies are sometimes preferred, although polyclonal antibodies also can be employed.

More particularly, antibodies can be prepared by immunizing a mammal with a purified SYNGAP or preferably an immunogenic peptide thereof such as those peptides specifically described below. The SYNGAP or SYNGAP peptide can be administered to the mammal alone or complexed with a carrier. Suitable mammals include typical laboratory animals such as sheep, goats, rabbits, guinea pigs, rats and mice. Rats and mice, especially mice, are preferred for obtaining monoclonal antibodies. The antigen can be administered to the mammal by any of a number of suitable routes such as subcutaneous, intraperitoneal, intravenous, intramuscular or intracutaneous injection. The optimal immunizing interval, immunizing dose, etc. can vary within relatively wide ranges and can be determined empirically based on this disclosure. Typical procedures involve injection of the antigen several times over a number of months. Antibodies are collected from serum of the immunized animal by standard techniques and screened to find antibodies specific for the SYNGAP. Monoclonal antibodies can be produced in

cells which produce antibodies and those cells used to generate monoclonal antibodies by using standard fusion techniques for forming hybridoma cells. See G. Kohler, et al., *Nature*, 256:456 (1975). Typically this involves fusing an antibody producing cell with an immortal cell line such as a myeloma cell to produce the hybrid cell. Alternatively, monoclonal antibodies can be produced from cells by the method of Huse, et al., *Science*, 256:1275 (1989).

One suitable protocol provides for intraperitoneal immunization of a mouse with a composition comprising purified immunogenic SYNGAP peptide such as those specifically disclosed below conducted over a period of about two to seven months. Spleen cells then can be removed from the immunized mouse. Sera from the immunized mouse is assayed for titers of antibodies specific for the immunogenic SYNGAP peptide prior to excision of spleen cells. The excised mouse spleen cells are then fused to an appropriate homogenic or heterogenic (preferably homogenic) lymphoid cell line having a marker such as hypoxanthine-guanine phosphoribosyltransferase deficiency ($HGPRT^-$) or thymidine kinase deficiency (TK^-). Preferably a myeloma cell is employed as the lymphoid cell line. Myeloma cells and spleen cells are mixed together, e.g. at a ratio of about 1 to 4 myeloma cells to spleen cells. The cells can be fused by the polyethylene glycol (PEG) method. See G. Kohler, et al., *Nature*, *supra*. The thus cloned hybridoma is grown in a culture medium, e.g. RPMI-1640. See G. E. More, et al., *Journal of American Medical Association*, 199:549 (1967). Hybridomas, grown after the fusion procedure, are screened such as by radioimmunoassay or enzyme immunoassay for secretion of antibodies that bind specifically to the purified SYNGAP or the immunogenic SYNGAP polypeptide. Preferably an ELISA is employed for the screen. Hybridomas that show positive results upon such screening can be expanded and cloned by limiting dilution method. Further screens are preferably performed to select antibodies that can bind to SYNGAP or the immunogenic SYNGAP peptide in solution as well as in a mammalian fluid sample such as those obtained from a human. The isolated antibodies can be further purified by any suitable immunological technique including affinity chromatography.

For human therapeutic applications, it may be desirable to produce chimeric antibody derivatives, e.g. antibody molecules that combine a non-human animal variable region and a human constant region, to thereby render the antibodies less immunogenic in a human subject than the corresponding non-chimeric antibody. A variety of types of such chimeric antibodies can be prepared, including e.g. by producing human variable region chimeras, in which parts of the variable regions, especially conserved regions of the antigen-binding domain, are of human origin and only the hypervariable regions are of non-human origin. See also discussions of humanized chimeric antibodies and methods of producing same in S.L. Morrison, *Science*, 229:1202-1207 (1985); Oi et al., *BioTechniques*, 4:214 (1986); Teng et al., *Proc. Natl. Acad. Sci. U.S.A.*, 80:7308-7312 (1983); Kozbor et al., *Immunology Today*, 4:7279 (9183); Olsson et al., *Meth. Enzymol.*, 9:3-16 (1982). Additionally, transgenic mice can be employed. For example, transgenic mice carrying human antibody repertoires have been created which can be immunized with SYNGAP or the immunogenic SYNGAP peptide. Splenocytes from such immunized transgenic mice can then be used to create hybridomas that secrete human monoclonal antibodies that specifically react with the SYNGAP or immunogenic SYNGAP peptide. See N. Lonberg et al., *Nature*, 368:856-859 (1994); L.L. Green et al., *Nature Genet.*, 7:13-21 (1994); S.L. Morrison, *Proc. Natl. Acad. Sci. U.S.A.*, 81:6851-6855 (1994).

As described previously, an antibody of this invention (polyclonal or monoclonal) or antigen-binding fragment thereof can be specifically bound to SYNGAP, e.g., in an excitatory chemical synapse. Thus, a pharmaceutical composition containing the antibody and particularly a monoclonal antibody in a pharmaceutically acceptable carrier or diluent is useful for the detection or diagnosis of cells comprising SYNGAP, e.g., neurons and other cells which may use SYNGAP as a marker such as tumors derived from neurons.

To faciliate detection or diagnosis, the desired antibody will usually be detectably-labeled. A wide spectrum of labels are known in the field such as those that

can be readily detected following administration to a subject and particularly a human patient. However, a radioisotope can be desirably used as a label because such labels are usually well suited to use in diagnostic imaging, especially those methods using scintigraphy or related methods. Choice of label will depend on several parameters the half-life or particle desired and the purpose of the detection or diagnosis. In many cases, it will be useful to choice a radionuclide that can be stored in a target tissue such as ^{99}Tc and other suitable radionuclides.

For *in vivo* administration, nearly any kind of carrier or diluent, preferably a pharacuetically acceptable carrier or diluent is acceptable and can be used for preparation of the pharmaceutical composition of the present invention. It is also possible to use a plurality of carriers or diluents in combination. It is desirable to use a sterile and aqueous isotonic suspension or solution including, for example, a physiological saline and a phosphate buffer physiological saline. The pharmaceutical composition of the present invention can be administered by non-oral administration such as subcutaneous administration, intramuscular administration, intravenous administration, intraperitoneal administration, or other routes as discussed above. Preferred amounts of the pharmaceutical composition to be administered include those specific amounts discussed above.

Additonally, suitably labelled antibodies and antigen-binding fragments that bind SYNGAP or SYNGAP-related molecules can be used in vito, e.g., in tissue culture, to detect excitatory chemical synapses in developing or established neuronal cell cultures. In this example, the antibody can be detectably-labeled with a variety of labels known in the field.

By the term "specific binding" or similar term is meant a molecule disclosed herein which binds another molecule, thereby forming a specific binding pair, but which does not recognize and bind to other molecules as determined by, e.g., Western blotting,

ELISA, RIA, gel mobility shift assay, enzyme immunoassay, competitive assays, saturation assays or other suitable protein binding assays known in the field.

As specifically shown in the examples which follow, we have isolated a novel Ras-GTPase activating protein called SYNGAP. The SYNGAP protein specifically interacts with the PDZ domains of PSD-95 and SAP102 *in vitro* and *in vivo*. SYNGAP is selectively expressed in brain and is highly enriched at excitatory synapses where it is present in a large macromolecular complex with PSD-95 and the NMDA receptor. SYNGAP stimulates the GTPase activity of Ras suggesting that it negatively regulates Ras activity at excitatory synapses. Ras signaling at the postsynaptic membrane may be involved in the modulation of excitatory synaptic transmission by NMDA receptors and neurotrophins. These results indicate that SYNGAP may play an important role in the modulation of synaptic plasticity.

In particular, the examples below show that SYNGAP is a brain-specific protein of about 125 kDa that is associated in a large complex with PSD-95/SAP90, SAP102, and the NMDA receptor in brain. Immunocytochemical studies show that SYNGAP is highly enriched at excitatory synapses and colocalizes with PSD-95/SAP90, SAP102, and the NMDA receptor. The GTPase activating domain shares significant homology with other rasGAPs and has rasGAP activity. These results suggest that the PSD-95/SAP90 family, through SYNGAP, may play a role in the regulation of synaptic ras signal transduction cascades.

The following non-limiting examples are illustrative of the present invention.

The following Examples 1-8 refer to the isolation and characterization of SYNGAP-c (GAPSYN) unless otherwise specified.

EXAMPLE 1- Molecular Characterization of SYNGAP

Novel proteins that interact with the PDZ domains of the PSD-95/SAP90 family of proteins were identified by using the third PDZ domain of SAP102 to screen a yeast two-hybrid hippocampal cDNA library (Fields, S. and Song, O. (1989) *Nature.* 340:245; Dong, H., et al., (1997) *Nature.* 386:279). Screening two million clones led to the isolation of a single clone with an open reading frame of 168 amino acids. Successive screening of a λZAP hippocampal cDNA library yielded several full length cDNAs with insert sizes of ~7.4 kb. The full length cDNA had an open reading frame encoding 1135 amino acids with a calculated molecular weight of 124.7 kDa. See Figures 3A- D; and Figures 4A-B.

Analysis of the amino acid sequence of the protein indicates that it is novel and contains several functional domains (Figure 4B) . The amino terminal half of the protein includes a region that has some homology to PH (pleckstrin homology) domains, a C2 domain that may be involved in the binding of Ca^{2+} and phospholipid, and a rasGAP domain. The C-terminal half includes a repeat of 10 histidines which may be involved in metal chelation, several potential serine and tyrosine phosphorylation sites and a T/SXV motif (QTRV) required for the interaction with SAP102 and PSD-95 (see below). The amino acid sequence also predicts that it is a cytosolic protein that has no apparent transmembrane region and no signal peptide. Alignment of the GAP domain of SYNGAP with other ras-GAPs (Figure 1C) indicates that the amino acids are critical for the interaction of rasGAPs with Ras and the stimulation of Ras GTPase activity are conserved (Scheffzek, K., et al. (1997) *Science.* 277:333). Because of its ras-GTPase activity and selective localization at excitatory synapses (see below), this protein was named SYNGAP.

Figures 4A-C are more particularly described as follows: Figure 4A: amino acid sequence of SYNGAP (SEQ ID NO. 21). SYNGAP is a 1135 amino acid protein that contains a ras-GAP domain (shaded) and several regulatory domains. Consensus serine and tyrosine phosphorylation sites are underlined. Figure 4B: In addition to the ras-GAP

domain (GAP) the structure of SYNGAP includes a domain that shares a partial homology to PH domains (PH) followed by a C2 domain (C2). The C-terminal four amino acids (QTRV) required for binding to PDZ domains are indicated. Figure 4C: alignment of the ras-GAP domain of SYNGAP with *Rattus norvegicus* (rn) ras-GAP (L13151) and *Homo sapiens* neurofibromin (hs 1NF1, M38107). Identical residues are in bold type. The residues that participate in catalysis (*) and in the interaction with Ras (+) are indicated.

1. Identification and Cloning of SYNGAP

The yeast two-hybrid system was utilized to find protein(s) that interact with the third PDZ domain of SAP102. The third PDZ domain (amino acids 367 to 452) was generated by PCR using a pair of oligonucleotides with restriction digestion sites for *Sal* I and *Bgl* II sense (5'-ACGCGTCGACCAGAGAGCCCCGCAAG-3' (SEQ ID NO. 22)) and antisense (5'-GAAGATCTAGGTCTATACTGGGCCAC-3' (SEQ ID NO. 23)) and was subcloned into the pPC97 yeast vector containing the GAL4 DNA binding domain (Chevray, P. M., and Nathans, D. (1992) *Proc. Natl. Acad. Sci. USA*. 89:5789). The bait plasmid was then transformed into Y190 yeast cells (Durfee, T., et al. (1993) *Genes Dev.* 7:555; Staudinger. J., et al. (1995) *J. Cell Biol*. 128:263) and a two-hybrid screening was performed using a random-primed cDNA library from rat hippocampus subcloned into the *Sal* I /*Not* I site of the pPC86 vector containing the GAL 4 transcription activation domain (Brakeman, P. R., et al. (1997) *Nature*. 386:284; Dong et al., *supra*). Positive clones were selected on plates lacking leucine, tryptophan, and histidine with 50 mM 3-aminotriazole and confirmed by filter assay for β-galactosidase activity (Breeden, L., and Nasmyth, K. (1985) *Cold Spring Harb. Symp. Quant. Biol.* 50: 643). For cloning of the full length of SYNGAP, successive rounds of phage library screening were performed with rat hippocampal λZAP cDNA libraries (dT-primed and random-primed). The nucleic acid sequence of the SAP102 protein can be found in Mueller, et al. (1996) *Neuron*. 17:255. the hippocanpal λ ZAP cDNA library was made according to standard methods. See e.g., Ausubel et al. *supra* and Sanbrook et al., *supra*.

1. Transfection of HEK 293T Cells

SYNGAP subcloned into pGW- 1 mammalian expression vector (10 μg) was transfected into HEK 293T cells in 10 cm culture dishes by calcium phosphate co-precipitation (Blackstone, C. D., et. al. (1992) *J. Neurochem.* 58:1118). After 48 hours of transfection the cells were harvested and analyzed by SDS-PAGE and immunoblotting.

EXAMPLE 2- Interaction of SYNGAP and PDZ domains Inside Cells

The interaction of SYNGAP with the PDZ domains of PSD-95/SAP90 and SAP102 was further studied in the yeast two-hybrid system. As shown in Table 1 below, SYNGAP interacts with all of the PDZ domains of PSD-95/SAP90. Deletion analysis of SYNGAP's C-terminus revealed that the C-terminal -TRV is critical for binding of SYNGAP to the PDZ domains (Table 1). In addition, the last valine residue is essential for interaction, as has been shown with other ligands for the PSD95/SAP90 family of proteins.

1. Yeast Interaction Studies

The yeast two-hybrid system was used to check for interaction of the carboxy terminal tail of SYNGAP with the various PDZ domains of SAP102 and PSD-95/SAP90. The PDZ domains of PSD-95/SAP90 and SAP102 were amplified by PCR and subcloned into the yeast vector, pPC 86. PDZ domain 1 of PSD-95 covers the amino acids from 40 to 160; PDZ domain 2, from 156 to 248; and PDZ domain 3, from 298 to 403. See e.g., Cho et al., (1992) *Neuron* 9:929 for disclosure relating to the PSD-95 sequence.

The original yeast clone with the intact C-terminal tail of SYNGAP (968- 1136) was subcloned into pPC97 and was used to check for interaction with the various PDZ domains. The requirement of the C-terminal T/SXV motif was investigated by subcloning PCR generated deletion mutants of SYNGAP (894 to 1134 for -QTR* and 894 to 1132 for -Q*). The yeast vectors are transformed into Y190 and scored by growth without

leucine, tryptophan, and histidine, in 100 mM 3-aminotriazole and filter assay for β-galactosidase activity.

Table 1 PDZ Domain Interaction with the Carboxy Terminal Tail Motif, -QTRV, of SYNGAP

	(-QTRV*)		(-QTR*)		(-Q*)	
	HIS3	B-Gal	**HIS3**	**B-Gal**	**HIS3**	**B-Gal**
SAP102						
PDZ 3	+	+	-	-	-	-
PSD-95						
PDZ 1	+	+				
PDZ 2	+	+				
PDZ 3	+	+				

EXAMPLE 3- Brain-Specific Expression of SYNGAP mRNA and Protein

Northern blotting with the *Sal* I / *Not* I fragment of the yeast clone revealed a mRNA of approximately 7 kb which was detected only in brain and was expressed predominantly in cortex, hippocampus, and olfactory bulb (Figure 7A). In addition, a less abundant mRNA of about 9 kb was observed in these same tissues. To characterize the SYNGAP protein, an anti-SYNGAP antibody was generated against its last C-terminal 20 amino acids (Figure 7B). The anti-SYNGAP C-terminal antibody specifically recognized 130 kDa SYNGAP protein when it was expressed in HEK 293 cells. In brain, the anti-SYNGAP antibody recognized a doublet or triplet of proteins at 130 kDa (Figure 7C). Preabsorption of the anti-SYNGAP antibody with the peptide immunogen completely eliminated the recognition of the 130 kDa protein confirming the specificity of the antibody. The origin of the triplet in brain is not entirely understood. Without wishing to be bound to any specific theory, the triplet may arise from alternative splicing

or posttranslational modification. Using the anti-SYNGAP antibody, the expression of SYNGAP in different tissues was examined. As with the Northern blot data. SYNGAP protein was found to be expressed exclusively in brain with high levels in the cortex and hippocampus and relatively low levels in cerebellum (Figure 7C). SYNGAP was found to be selectively localized to membrane fractions and was resistant to Triton X-100. CHAPS. and RIPA extractions from synaptic plasma membranes (Figure 7D) similar to other proteins associated with the PSD such as PSD-95/SAP90, SAP102, and the NMDA receptor (Cho, K.O., et al. (1992) *Neuron*. 9:929; Lau et al., *supra* 1996; Kim, E., et al. (1997) *J. Cell. Biol.* 136:669).

Figures 7A- 7D are more specifically described as follows: Figure 7A Northern blot of SYNGAP mRNA shows high level of SYNGAP mRNA expression in brain. Figure 7B: antibodies were generated against SYNGAP and used to identify SYNGAP in rat tissues using immunoblot techniques. These antibodies recognized a 130kDa protein in HEK293T cells transfected with the SYNGAP cDNA (Lane 2) and in rat brain homogenates (Lane 3). The 130kDa protein was not detected in mock transfected HEK293T cells (lane 1) and immunorecognition of the 130kDa protein in brain was blocked by preabsorbtion of the antibody with the antigen (Lane 4). Figure 7C: immunoblots of rat tissues with the SYNGAP antibody demonstrates that the expression of the SYNGAP protein is brain specific. Figure 7D: immunoblots of rat brain cortex crude homogenates (cortex) and cytosolic and membrane fractions demonstrate that SYNGAP is membrane-associated. Cortical membranes were extracted with the indicated detergents and then separated into soluble (S) and pellet fractions (P) and the distribution of SYNGAP detected using immunoblot techniques. SYNGAP is resistant to membrane extraction with non-denaturing detergents similar to other proteins located in the PSD fraction.

1. RNA Preparation and Northern Blot Analysis

Total RNA from various tissues of male Sprague Dawley rat at P14 was isolated with RNAzol (Tel-Test) according to the manufacturer's protocol. The RNA (10 μg per

lane) was separated on 1.2% formaldehyde agarose gel, transferred onto GeneScreen Plus membrane (Du Pont NEN) and then hybridized with a [α-^{32}P]-dCTP labeled *Sal* I */Not* I fragment of the original yeast clone. The result was visualized using a phosphoimager cassette. The blot was stripped and rehybridized with radioactively labeled GAPDH *(Hind* III/*BamH* I fragment) DNA to ensure equal loading of RNA per lane.

EXAMPLE 4- SYNGAP Associates with PSD-95 and SAP102 *in vivo*

Interaction of SYNGAP, PSD-95/SAP90 and SAPlO2 was examined in the brain *in vivo*. As shown in Figure8, immunoprecipitation of PSD-95/SAP90 or SAP102 from deoxycholate solubilized brain membrane preparations resulted in the specific coimmunoprecipitation of SYNGAP. Moreover, using antibodies to the NRl subunit of the NMDA receptor, SYNGAP was also found to be specifically associated with NMDA receptors (Figure 8). Preabsorption of the SAPl02 and NRl antibodies with their antigens blocked the coimmunoprecipitation of SYNGAP confirming the specificity of the association. In contrast, SYNGAP did not coimmunoprecipitate with the NMDA receptor GluRl subunit. These results strongly suggest that SYNGAP was associated with an NMDA receptor complex containing NMDA receptor subunits and PSD-95/SAP90 family members.

Figure 8 is more specifically described as follows: Synaptic plasma membranes were solubilized with deoxycholate and the resulting deterrent extract (input) was used to immunoprecipitate the indicated proteins (IP). The immunoprecipitates were then analyzed for the presence of SYNGAP, NMDAR1, PSD-95 and GluR1 by immunoblot techniques as indicated above.

1. Brain Membrane Preparation and Solubilization

Membrane preparations (P2) and solubilization was carried out according to the procedures described by Luo et al. (1997) with modifications. Cortex and hippocampus from a male Sprague-Dawley rat, age of 4 to 6 weeks were homogenized twice using a

glass-Teflon homogenizer with protease inhibitors (antipain, chymotrypsin, leupeptin, Trasylol, 0.1 mM PMSF). After determining the protein concentration of the P2 fraction by a Coomasie assay (Pierce), aliquots of the proteins at 3 mg/ml were stored at -80°C until use. For coimmunoprecipitation, PA (300 µg per IP) was solubilized by 1.0 % sodium deoxycholate followed by 0.1 % Triton X-100 and the preparation was centrifuged for 10 minutes at 100,000 x *g*. The supernatant was then used for coimmunoprecipitation.

For detergent extraction of SYNGAP, synaptic plasma membranes were prepared and solubilized using various detergents, SDS, Triton X-100, CHAPS, and RIPA, according to the procedure described by Lau et al. *supra*.

EXAMPLE 5- Detection of SYNGAP at Specific Synapses

The subcellular distribution of SYNGAP in neurons was examined in low density hippocampal cultures using the anti-SYNGAP antibody. SYNGAP was expressed in the cell body of neurons but the pattern of immunoreactivity was strikingly punctuate along the processes of the neurons, suggesting that SYNGAP may be localized to synapses (Figure 9A). Double labeling the hippocampal neurons with antibodies against SYNGAP and the synaptic marker protein synaptophysin demonstrated that SYNGAP is specifically localized to synapses (Figures 9B- 9D). The staining of the neurons with the SYNGAP antibody was blocked by preabsorption of the antibody with the antigenic peptide confirming the specificity of the antibody (Figures 9E-9F).

As noted above in Example 3, SYNGAP associated with PSD-95 and SAP102 *in vivo*. Next, the colocalization of the PSD95/SAP90 family members with SYNGAP was examined. It was found that SYNGAP colocalized with PSD-95 (Figure 10A-10I). This observation provides additional support for SYNGAP association with PSD-95.

To determine whether SYNGAP is localized to both excitatory and inhibitory synapses, neurons were double labeled with SYNGAP antibodies and antibodies against the NR1 subunit of the NMDA receptor to label excitatory synapses or anti-glutamatic acid decarboxylase (GAD) antibodies to label inhibitory synapses. As shown in Figure 5B SYNGAP colocalized with NMDA receptors and was present at all excitatory synapses. In contrast, SYNGAP was not observed at GABAergic synapses (Figure 10G-10I).

Figures 9A- 9F are more particularly explained as follows: Figure 9A: low density hippocampal cultures were stained with the SYNGAP antibody and visualized with a Rhodamine-coupled secondary antibody. SYNGAP is present in the cell soma and is clustered on the neuronal processes. Figures 9B-9D: double labeling of the hippocampal cultures with antibodies against SYNGAP and the synaptic marker synaptophysin demonstrates that SYNGAP is synaptically localized. Figures 9E-9F: the staining of the hippocampal neurons with the SYNGAP antibody is specifically blocked by preincubation of the antibody with the antigen. The right panel shows that the double labeling with anti-synaptophysin antibody is not blocked by the SYNGAP antigen.

Figures 10A -10I are also more particularly described as follows: Figure 10A-10C: double labeling of hippocampal neurons with antibodies against SYNGAP and PSD-95 demonstrates that SYNGAP and PSD-95 are colocalized in the neurons. Figure 10D-10F: SYNGAP exists exclusively at excitatory synapses as shown by the colocalization of SYNGAP with the NR1 subunit of the NMDA receptor. Figures 10G-10I: to exclude the possibility that SYNGAP is found at inhibitory synapses, the hippocampal neurons were double labeled with the antibodies to SYNGAP and the GABAergic synaptic marker GAD. GAD staining does not overlap with the expression pattern of SYNGAP.

EXAMPLE 6- SYNGAP has Ras-GAP Activity

SYNGAP shows homology with the GAP domain of rasGAPs suggesting that SYNGAP may regulate the GTPase activity of Ras (Boguski and McCormick, (1993) Nature 366: 643). A glutathione S-transferase (GST) fusion protein of the rasGAP domain of SYNGAP was made and incubated with a purified H-ras GST fusion protein in the presence of [γ-^{32}P]-GTP. It was found that GST-ras fusion proteins exhibited a low intrinsic GAP activity in the absence of a rasGAP (Figure 11). In contrast, addition of the GST fusion protein of the GAP domain of SYNGAP dramatically stimulated the GTPase activity of Ras (Figure 11). Control GST-backbone protein (Figure 11) or a GST-SAP102 fusion protein had no effect on ras-GTPase activity.

1. Fusion Protein Construction and Preparation

The first 119 amino acids of SAPl02 was amplified by PCR and subcloned in frame into pTrcHisB vector (Invitrogen) via the *BamH* I and *EcoR* I restriction digest sites. The construct was then transformed into BL2l bacteria and following an induction of expression with IPTG. The protein was purified in a denaturing condition according to the protocol provided by the QIA-expressionist (Qiagen). The GAP domain (266-52l) subcloned into pGEX-4T2 and a GST-Ras fusion protein was obtained and expressed in BL2l cells. The fusion protein was purified using glutathione coupled agarose. All of the above proteins were analyzed by SDS-PAGE followed by Coomassie Blue Staining.

2. GAP Assay

The GAP assay was performed following the methods described by Settleman et al. (1992) *supra* with modifications. Briefly, 0.5 to 1 μM of GST-Ras was incubated with 20 nM [γ-^{32}P]-GTP (6,OOO Ci/mmol, Du Pont-NEN) in 50 mM Tris, pH 7.5, 50 mM NaCl, 1 mM EDTA, 1 mg/ml BSA, and 1 mM DTT for 10 minutes at room temp. GST-GAP or control GST fusion protein (200 ng) was then added in 50 mM Tris, pH 7.5, 5 mM $MgCl_2$, 1 mhI DTT and incubated for the indicated times. Atter stopping the reaction (by adding 5 volumes of ice-cold 50 mM Tris, pH 7.5, 5 mM $MgCl_2$; 1 mM

DTT), the mixture was filtered through HA membranes (Millipore) and the filters were counted for ^{32}P in scintillation cocktail.

Results of the GAP assay are shown in Figure 11. Time course of the GTPase activity of GST H-Ras fusion protein in the presence and absence of the GAP domain of SYNGAP. Incubation of a GST-ras fusion protein with a control GST fusion protein (--◊--) had little effect on the slow intrinsic GTPase activity or GST-Ras. In contrast, addition of the GST-fusion protein containing the GAP domain of SYNGAP dramatically stimulated the GTPase activity of GST-Ras (-□-).

EXAMPLE 7- Generation and Purification of SYNGAP and SAP102 Antibodies

The last 20 amino acids of SYNGAP (KRLLDAQRGSFPPWVQQTRV (SEQ ID NO. 21) were synthesized and purified. The protocol for generation and purification of polyclonal antibody was described by Blackstone et al. (Blackstone et al., 1992 *supra*). Briefly, the peptide was crosslinked to thyroglobulin with glutaraldehyde and injected into New Zealand white rabbits to generate antiserum (Covance). The antiserum was then purified with Affi-Gel 10 resin (Bio-Rad) coupled to BSA covalently bound to the peptides (Lau et al., (1996), *supra*). The N-terminal SAP102 fusion protein with hexahistidine tag was immunized similarly to generate a polyclonal rabbit antibody and the antiserum was purified using the antigen coupled to Affi-Gel 10.

1. Coimmunoprepitation and Immunoblotting

To affinity purified antibodies, about 1 to 2 µg were preincubated with 50 µl of 1:1 slurry of protein A-Sepharose for 1 hour and the protein A-antibody complex was spun down at 2000 rpm for 2 minutes. The clarified supernatant of solubilized P2 fraction was then added to the sepharose beads and the mixture incubated for 2 to 3 hours at 4° C. The mixture was washed once with 1% Triton X-100 in immunoprecipitation buffer (137 mM NaCl, 2.7 mM KCl, 4.3 mM Na_2HPO_4, 1.4 mM KH_2PO_4, 5 mM EDTA, 5 mM EGTA, 1 mM sodium vanadate. 10 mM sodium pyrophosphate, 50 mM NaF, 20 units/ml

Trasylol and 0.1 mM phenylmethylsulfonyl fluoride), twice with 1 % Triton X-100 in immunoprecipitation buffer plus 300 mM NaCl, and three times with immunoprecipitation buffer. The proteins were eluted by Laemmli sample buffer (Laemmli, 1970) and were separated by SDS-PAGE. The gel was transferred to a PVDF (Millipore) membrane and the membrane was blocked and immunoblotted as described by Lau et al. (1996), *supra*. When the antibodies were blocked with antigens, they were preincubated with the peptide at concentration of 100 μg/ml or fusion proteins at concentration of 50 μg/ml. The antibodies used in the experiments have been previously described: anti-NRIa C-terminal antibody (Tingley, W. G., et al. (1993) *Nature.* 364:70), anti-GluRl C-terminal antibody (Blackstone et al., 1990), anti-NR2B C-terminal antibody (Lau, L. F., and Huganir, R. L. (1995) *J. Biol. Chem.* 270:20036), and anti-PSD-95 antibody (Gift from Dr. J. S. Trimmer)

2. Immunocytochemistry

Low density hippocampal neuronal culture was performed following the procedure described by Goslin and Banker (Goslin and Banker, 1991). After 13 to 90 days in culture, the neurons were fixed and stained with affinity purified antibodies as previously described with minor modifications (Lau and Huganir, 1995 *supra*; O'Brien, R. J., et al. (1997) *J. Neurosci.* 17:7339; Rao, A. and Craig, M. (1997) *Neuron.* 19:801).

Examples 1 to 8 show the isolation and characterization SYNGAP, a novel synaptic rasGAP that directly interacts with the PSD-95/SAP90 family of proteins. SYNGAP is highly expressed in brain, is not detected in other tissues and is especially abundant in the cortex, hippocampus, and olfactory bulb. SYNGAP is found exclusively at excitatory synapses in hippocampal neurons in culture. The SYNGAP protein is tightly associated with synaptic membranes, and exists as two or more alternate forms. Due to its synaptic localization and association with the PSD it is uniquely positioned to regulate signal transduction events that may involve ras signaling pathways at excitatory synapses.

EXAMPLE 8- Isolation of Human SYNGAP

It is possible to isolate *Homo sapiens* SYNGAP in accord with the present disclosure. For example, in one approach, the SYNGAP can be obtained by screening a human brain cDNA γZAP phage library (Stratagene) at high stringency conditions. More particularly, the hybridization can be carried out by incubation at 65°C overnight in 0.08 Na phosphate, pH 6.8, 0.05 mNa citrate, 0.5 mNaCl, 5X Denhardt's solution, 0.5% SDS, 0.1 mg/ml salmon sperm DNA with a probe concentration of about 0.4 million CPM/ml. A preferred probe can be made by standard methods from any of the *Rattus norvegicus* SYNGAP DNA sequences shown in SEQ ID Nos. 1-2, 4-5, or 7-8. Especially preferred probes have a length between about 500 to about 2000 bases. Such probes are typically restriction fragments that can be readily obtained by restriction enzyme digestion of a desired SYNGAP cDNA followed by purification of the fragment. Typically, the fragment is detectably-labeled, e.g., with ^{32}P to facilitate screening. The homology of the clone isolated between the two different species (i.e. rat and human) can be compared: an identity of 70 to 80% may be observed at the DNA sequence level. At the protein, about 70 to about 90% identity may be observed across a substantial length of the human gene. The isolated human clone can be analyzed in accordance with the SYNGAP sequences disclosed herein to identify mRNA expression pattern, GAP activity, and/or participation in a MAP kinase cascade.

The examples also show that SYNGAP has an organized and domain structure which is involved in the regulation of its GAP activity. In addition to the ras-GAP domain the amino terminus contains a region that is partially homologous to pleckstrin homology (PH) domains, a phospholipid binding module of about 100 amino acids that binds polyphosphatidylinositides which is thought to serve as a signal dependent membrane adaptor (Shaw, G. (1996) *Bioessays.* 18:35). The N-terminal region also contains a C2 domain which has been shown to be involved in the binding of Ca^{2+} in a phospholipid-dependent manner (Luo, J. H., and Weinstein, I. B. (1993) *J. Biol. Chem.* 268:23580) in protein kinase C, synaptotagmin and rabphilin-3A (Nishizuka, Y. (1988)

Nature. 334:661; Perin, M. S., et al. (1991) *J. Biol. Chem.* 266:623; Yamaguchi, et al., (1993) *J. Biol. Chem.* 268:27164). C2 domains have also been found in other rasGAPs such as human p120GAP and GAP1^{IP4BP} (Cullen. P.J., et al. (1995) *Nature.* 376:527). The presence of these two domains suggests that SYNGAP may respond to changes in Ca^{2+} and phospholipid second messengers. The association of SYNGAP with the NMDA receptor complex suggests that SYNGAP may specifically respond to changes in Ca^{2+} mediated by activation of NMDA receptors. The C-terminal half of SYNGAP also contains potential regulatory domains including many consensus phosphorylation sites for CaMKII and protein tyrosine kinases. CaMKII is very abundant in the postsynaptic density and has been implicated as having a key role in the modulation of synaptic plasticity (Nicoll, R.A. and Malenka, R.C. (1995) *Nature.* 377:115). In addition. SYNGAP has ten consecutive histidine residues which may bind divalent transition metals such as Zn^{2+} and Cu^{2+} and play some role in the regulation of SYNGAP function.

The *in vivo* association of SYNGAP with the NMDA receptor complex and PSD-95 and SAP 102 suggests that SYNGAP plays a specific role in the modulation of ras signaling at excitatory synapses. The specific localization of SYNGAP to excitatory synapses suggests that SYNGAP may play a critical role in the regulation of BDNF signaling in the postsynaptic membrane.

The identification of SYNGAP as a PSD-95 associated protein provides the first evidence that the PSD-95/SAP90 family forms a complex with signal transduction molecules involved in the ras pathway and suggest that ras plays specific roles in the regulation of excitatory synaptic transmission at the postsynaptic membrane. SYNGAP may also regulate ras signaling in response to Ca^{2+}.

The invention has been described in detail with reference to preferred embodiments thereof. However, it will be appreciated that those skilled in the art, upon consideration of this disclosure, may make modification and improvements within the spirit and scope of the invention as set forth in the following claims.

All references and patent publications cited herein are fully incorporated herein by reference.